

(TM)

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Run on: Sat Jan 9 09:33:03 1999; MasPar time 1049.47 Seconds
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Tabular output not generated.

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Title: >US-08-704-178-1
Description: (1-712) from US08704178.seq (1 of 4)
Perfect score: 712
N.A. Sequence:
Comp: 1 ATGACCTGACAGTCACCA ..... GGACACAGTCACCGTCC 712
TACCTGACGTCGATGGGT ..... CCTGTGCACGTGCACAGG

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Scoring table: TABLE default
Gap 6

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Nmatch      STD :      Dbase 0; Query 0
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searched: 567134 seqs, 1101898692 bases x 2

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Post-processing: Minimum Match 08
                  Listing first 45 summaries
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Database:
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1:em_ba 2:em_fun 3:em_htg 4:em_hum1 5:em_hum2 6:em_in
7:em_com 8:em_or 9:em_ov 10:em_pat 11:em_ph 12:em_pi
13:em_ro 14:em_v1
genbank107
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15:gb_dgal16:gb_daz17:gb_htg18:gb_in19:gb_om20:gb_ov
21:gb_pat22:gb_ph23:gb_pil124:gb_pil25:gb_pr1
26:gb_pr227:gb_pr328:gb_ro29:gb_st30:gb_sts31:gb_sy
32:gb_un33:gb_v1

Statistics: Mean 10.607; Variance 5.121; scale 2.071

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	7405	99.0	711	21	I32460	Sequence 1 from patent anti-erbB2 immunotoxi	0.00e+00
2	705	99.0	711	31	S39560	DNA encoding a signal	0.00e+00
3	410	57.6	720	21	E13589	Sequence 2 from patent	4.82e-29
4	375	52.7	720	21	I12407	Sequence 1 from patent	1.52e-28
5	363	51.0	732	21	I1035	CDNA encoding a monoc	1.52e-28
6	363	51.0	732	10	E10361	Mus musculus rearrange	7.59e-21
7	283	39.7	736	28	MWU37860	CDNA encoding an monoc	2.23e-20
8	279	39.2	729	10	E10362	Sequence 3 from patent	1.91e-20
9	279	39.2	729	21	I1036	Mus hybridoma 2d3 mr	1.40e-19
10	271	38.1	321	28	MWIG013	Sequence 2 from patent	1.40e-19
11	270	37.9	315	21	A36642	Sequence 3 from patent	7.55e-19
12	270	37.5	315	21	I1657	Ig V kappa -anti-Idiot	7.55e-19
13	268	37.6	312	28	S48339		

14	268	37.6	318.28	AF056217	Mus musculus monoclonal	7.55e-193
15	268	37.6	1370.28	MUSICKAR	Mouse Ig kappa active	7.55e-193
16	267	37.5	744.31	SYND44X	Synthetic single-chain	5.54e-191
17	266	37.4	354.28	S78745	Ig VH-anti-phosphatidy	4.07e-191
18	265	37.2	345.28	MUSICKA2A	Mouse hybridoma Ig re	2.98e-191
19	265	37.2	351.28	MUS25678	Mus musculus Ig heavy	2.98e-191
20	263	36.9	354.28	MMACHVR2	Mus musculus antibody	1.60e-191
21	263	36.9	403.28	MUSICKKCA	Mouse Ig rearranged ka	1.60e-191
22	263	36.9	403.21	I09200	Sequence 40 from Paten	1.60e-191
23	263	36.9	477.28	S76823	Ig V kappa -anti-sigma	1.60e-191
24	262	36.8	321.21	I27490	Sequence 4 from patent	1.17e-191
25	261	36.7	403.21	I05923	Sequence 39 from Paten	8.59e-191
26	260	36.5	355.28	S74055	IGG VH IIA-IgG2b VH re	6.29e-191
27	260	36.5	357.28	MUSCMVC	Mouse mRNA sequence, p	6.29e-191
28	260	36.5	414.21	I78572	Sequence 84 from paten	6.29e-191
29	260	36.5	414.21	I31560	Sequence 84 from paten	6.29e-191
30	260	36.5	414.21	I78627	Sequence 84 from paten	6.29e-191
31	259	36.4	421.28	S51851	M104E myeloma immunog	4.61e-191
32	258	36.2	309.28	MMICVR4	Mouse Ig active L-chain	3.37e-189
33	258	36.2	723.28	AF035617	Mus musculus scfv anti	3.37e-189
34	257	36.1	302.28	MUSICKRFE	Mus musculus Mouse Ig	2.47e-188
35	257	36.1	403.21	I08812	Sequence 14 from Paten	2.47e-188
36	257	36.1	617.31	XX057213	Synthetic construct c1	2.47e-188
37	255	35.8	327.28	AF087025	Mus musculus hybrid c2	1.32e-185
38	255	35.8	384.28	MM050285	Mus musculus BALB/c/J	1.32e-185
39	255	35.8	732.21	A51863	Sequence 27 from Paten	1.32e-185
40	254	35.7	321.28	MM060466	Mus musculus Ig anti-D	9.63e-186
41	253	35.5	435.21	A11967	Variable region of the	7.04e-185
42	252	35.4	300.28	MUSICKRFI	Mus musculus Ig active	5.14e-184
43	252	35.4	366.28	AF081541	Mus musculus anti-HIV-	5.14e-184
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45	251	35.3	440.28	MUSRA4	Mouse active H-chain v	3.75e-183

ALIGNMENTS

LOCUS	1	132406	711 bp	DNA	PAT	07-JAN-1997
DEFINITION	Sequence 1 from patent US 5587458.					
ACCESSION	132406					
NID	g1823197					
KEYWORDS	.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	Unclassified.					
AUTHORS	1 (bases 1 to 711)					
TITLE	King, C. Richier, Kasprzyk, P.G. and Bird, R.E.					
FEATURES	Anti-GrbB-2 antibodies, combinations thereof, and diagnostic uses thereof					
Journal	Patent: US 5587458-A 1 24-DEC-1996;					
Location/Qualifiers	Location/Qualifiers					
Source	1. 711					
BASE COUNT	175 a	182 c	190 g	164 t		
ORIGIN	/organism="Unknown"					
Query Match	99.0%, Score 705; DB 21; Length 711;					
Best Local Similarity	99.7%; Pred. No. 0.00e+00;					
Matches	710; Conservative	1; Mismatches	0; Indels	1; Gaps	1	
Db	1	ATGACCTGCAGCGTGACCAAGTCATCCAGCAATCTGTCTGCATCTCCAGGGAGAAAGT-	59			
QY	1	ATGGACCTGCAGCGTGACCAAGTCATCCAGCAATCTGTCTGCATCTCCAGGGAGAAAGTA	60			
Db	60	CACATAGACTTGCAGGGCCACCCCAAGTGAAGTTATATGACATGACATGGATATAGCAGAGCC	119			
QY	61	CACATAGACTTGCAGGGCCACCCCAAGTGAAGTTATATGACATGACATGGATATAGCAGAGCC	120			
Db	120	AGATCTCTCCCCCAACCTTGATTTATATACACATCCCAACCTGGCTTCTGAGATCCCTGC	179			
QY	121	AGATCTCTCCCCCAACCTTGATTTATATACACATCCCAACCTGGCTTCTGAGATCCCTGC	180			
Db	180	TCGGTTAGTGGGGGTGGTCTGGGACCTTTACTCTTCACAGTACGACGAGATGAGAGGC	239			

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181 TCGCTTACAGTGGCGGTGGTGGGACCTTACTCTCTCCAGCTCAGCAGAGTGGAGGC 240-
Db 240 TGAAGATGCTGCACTTATTTACTGCGACAGTGGAGTGTGCGCCACCGACTTGGAGG 299
Oy 241 TGAAGATGCTGCACTTATTTACTGCGACAGTGGAGTGTGCGCCACCGACTTGGAGG 300
Db 300 GGGGTCCAAAGCTGGAATAAAGGTTCTACCTGTGTTCTGTGTAATCTTCTGAAAGTAA 359
Oy 301 GGGGTCCAAAGCTGGAATAAAGGTTCTACCTGTGTTCTGTGTAATCTTCTGAAAGTAA 360
Db 360 AGGTGTGACGTGTCAGAGACTCAGACCTGAGGTGTGTAAGCTGTGAGTTAAAGAGAT 419
Oy 361 AGGTGTGACGTGTCAGAGACTCAGACCTGAGGTGTGTAAGCTGTGAGTTAAAGAGAT 420
Db 420 ATCTGCAAGACTTCTGGTTACTCATCTACCTGACACACATGAACTGGTGAAGCAGAG 479
Oy 421 ATCTGCAAGACTTCTGGTTACTCATCTACCTGACACACATGAACTGGTGAAGCAGAG 480
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Db 540 CAACCAAGAGTTCAGAGGCAAGGCCACATTTACTGTAAGCAAGTGTCCAGACAGCCTA 599
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Db 600 CATGAGCTCTCAGTCTCAGATCTGAGACTCTGAGCTATTTACTGTGCAAGAGAGGT 659
Oy 601 CATGAGCTCTCAGTCTCAGATCTGAGACTCTGAGCTATTTACTGTGCAAGAGAGGT 660
Db 660 TACGACTGTGACTTGCATGTCTGGGGCGCAGGGACCAAGGTCACCGTCTCC 711
Oy 661 TACGACTGTGACTTGCATGTCTGGGGCGCAGGGACCAAGGTCACCGTCTCC 712

RESULT 2 SYN 10-FEB-1993
LOCUS S39590 711 bp
DEFINITION anti-erbB2 immunotoxin antigen binding region [mice, other]
ACCESSION S39590
NID 9235113
KEYWORDS
SOURCE Mus sp.
ORGANISM Mus sp.
Eukaryota; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
VERTEBRATA;
REFERENCE 1 (bases 1 to 711)
AUTHORS Batta,J.K., Kasprzyk,P.G., Bird,R.E., Pastan,I. and King,C.R.
TITLES Recombinant anti-erbB2 immunotoxins containing Pseudomonas exotoxin
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89 (13), 5967-5971 (1992)
MEDLINE 92351198
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI glibseq 108547] from the original journal article.
This sequence comes from Fig. 1.
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1..711
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/translation="MDQLQSPAILASPFGEKVTWTCRATPSVSMHWYQOKPPSSP
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HGKMLEWIGLINPYNGDTNYNQKFKKATPTVKSSTAVMELLSLTSBSAVYCAR

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BASE COUNT 175 a 182 c 190 g 164 t
ORIGIN
Query Match 99.0%; Score 705; DB 31; Length 711;
Best local similarity 99.7%; Pred. No. 0.00e+00;
Matches 710; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
Db 1 ATGAGCTGACGTGACCCAGCTGCTCCAGCAATCTGTCTGCAATCTCCAGGGAGAAAGT- 59
Oy 1 ATGAGCTGACGTGACCCAGCTGCTCCAGCAATCTGTCTGCAATCTCCAGGGAGAAAGT 60
Db 60 CACAATGACTGAGGGGCCACCCCAAGTGAAGTTACATGCACTGGATATCAGACAGAGCC 119
Oy 61 CACAATGACTGAGGGGCCACCCCAAGTGAAGTTACATGCACTGGATATCAGACAGAGCC 120
Db 120 AGGATCTCCGCCCAACCTTGGATTATACACATCAATCAACCTGGCTTCTGAGTCCCTGC 179
Oy 121 AGGATCTCCGCCCAACCTTGGATTATACACATCAATCAACCTGGCTTCTGAGTCCCTGC 180
Db 180 TCGCTTCAAGTGGCGGTGGTCTGGACCTTCTACTCTCTCAGAGTACAGAGTGGAGGC 239
Oy 181 TCGCTTCAAGTGGCGGTGGTCTGGACCTTCTACTCTCTCAGAGTACAGAGTGGAGGC 240
Db 240 TGAAGATGCTGCCACTTATTAATGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGG 299
Oy 241 TGAAGATGCTGCCACTTATTAATGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGG 300
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Oy 301 GGGGTCCAAAGCTGGAATAAAGGTTCTTACCTGTGTTCTGTGTAATCTTCTGAAAGTAA 360
Db 360 AGGTGTGACGTGTCAGAGACTCAGACCTGAGGTGTGTAAGCTGTGAGTTAAAGAGAT 419
Oy 361 AGGTGTGACGTGTCAGAGACTCAGACCTGAGGTGTGTAAGCTGTGAGTTAAAGAGAT 420
Db 420 ATCTGCAAGACTTCTGGTTACTCATCTACCTGACACACATGAACTGGTGAAGCAGAG 479
Oy 421 ATCTGCAAGACTTCTGGTTACTCATCTACCTGACACACATGAACTGGTGAAGCAGAG 480
Db 480 CCATGGAAGAACTTGAAGTGGATTGAGCTTATTAATCCTTAACAATGGTATACTACTA 539
Oy 481 CCATGGAAGAACTTGAAGTGGATTGAGCTTATTAATCCTTAACAATGGTATACTACTA 540
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Oy 601 CATGAGCTCTCAGTCTCAGATCTGAGACTGCACTGATATTTACTGTGCAAGAGAGGT 660
Db 660 TACGACTGTGACTTGCATGTCTGGGGCGCAGGGACCAAGGTCACCGTCTCC 711
Oy 661 TACGACTGTGACTTGCATGTCTGGGGCGCAGGGACCAAGGTCACCGTCTCC 712

RESULT 3
LOCUS E13599 720 bp DNA PAT 27-APR-1998
DEFINITION DNA encoding a signal chain Fv antibody of anti-gp130 antibody
GPX7.
ACCESSION E13599
NID 93252401
KEYWORDS JP 1997220092-A/2.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 720)
AUTHORS Ekida,T., Yasukawa,K., Imanaka,T. and Takagi,M.
TITLES PRODUCTION OF SINGLE-STRAND FV ANTIBODY
JOURNAL Patent: JP 1997220092-A 2 26-AUG-1997;
TOSOH CORP
COMMENT OS None

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Db	420	AGTAACTCTCCGTGAAGGCTCTGTGGTAAACATTCACACACTCTACTGTGGATGCACCTGGGT	479
Qy	412		471
Db	480	GAAGCAGAGCATGAGACAAAGCCCTTGAAGTATGGATTGGAAATATTTATTCCTGGTAGTGATG	539
Qy	472	GAAGCAGAGCCATGGAAGAAGACCTTGAAGTATGGATTGACATTTAATTCCTTCAAAATGTGA	531
Db	540	TACTAACTAGGATGAGAGATTCAAGGCAAGGCGCACTAGCATGTGATGAGACACATCCTCCAG	599
Qy	532	TACTAACTAACCAACCAAGATTCAAGGGCAAGGCCACATTTACTGTGAGCAAAAGTCTCCAG	591
Db	600	CACAGCCTACATGCACCTCTGACAGCCTGCACATCTGAGAGACTCTGGGGTCTATTACTGTAC	659
Qy	592	CACAGCCTACATGAGAGCTCTCAGTCTGCACATCTGAGAGACTCTGCAAGTCTATTACTGTGC	651
Db	660	AAGAAGCAGCGCGAAGCTGGGTCTACATATG	688
Qy	652	AAGAAGGTTACGAGACTGTTACTTCATATG	680

FEATURES	7	16-MAR-1996
LOCUS	MMU37860	336 bp mRNA
DEFINITION	Mus musculus rearranged immunoglobulin heavy chain variable region mRNA, partial cds.	ROD
ACCESSION	U37860	
NID	91127634	
KEYWORDS		
SOURCE	house mouse.	
ORGANISM	Mus musculus.	
REFERENCE	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.	
AUTHORS	1. (bases 1 to 336) Gaton,A.J., Swartzentruber,J.R., Kuhl,A.L., Carding,S.R. and Stark,S.E.	
TITLE	Activation and negative selection of functionally distinct subsets of antibody-secreting cells by influenza hemagglutinin as a viral and a neo-self antigen	
JOURNAL	J. Exp. Med. 183 (1), 13-26 (1996)	
MEDLINE	96136744	
REFERENCE	2 (bases 1 to 336) Swartzentruber,J.R.	
AUTHORS	Direct Submission	
TITLE	Submitted (10-OCT-1995) Jennifer R. Swartzentruber, The Wistar	
JOURNAL	Institute, 3601 Spruce St., Philadelphia, PA 19104, USA	
LOCATION/Qualifiers	1..336	

CDS	<1.	.>336
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BASE COUNT	92 a	81 c	85 g	78 t
ORIGIN				

Query Match	95.7%	Score 283;	DB 281;	Length 336;
Best Local Similarity	95.1%	Pred. NO. 7,59e-211;		
Matches	309;	Conservative	0;	Mismatches 14; Indels 2; Gaps 2;

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QY	389	GAGGTGGGAAGCCTGTGAGGCTTCATTAAGATATATTCGCAAGCTTGTGTACTATTC	448

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ID	RESULT	8	standard; RNA; ROD; 729 BP.
OC	E10362		
AC	E10369		
NI	d1108699		
DT	08-OCT-1997 (Rel. 52, Created)		
DT	08-OCT-1997 (Rel. 52, Last updated, Version 1)		
DE	cDNA encoding an monoclonal antibody against human Interleukin-2		
DE	receptor gamma chain.		
KW	JP 1995313188-A/2.		
OS	Mus sp.		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia		
OC	Sciuromorphi; Muridae; Murinae; Mus.		
RN	[1]		
RP	1-729		
RA	Shimamura T., Hamuro J., Nakazawa H., Kanayama Y., Sugamura K.,		
RA	Takekoshi T.;		
RT	"IMMUNOSUPPRESSIVE AGENT";		
RT	Patent number JP 1995313188-A/2, 05-DEC-1995.		
RL	AJINOMOTO CO INC, SUGAMURA KAZUO.,		
CC	OS Mus sp. (mouse)		
CC	PN JP 1995313188-A/2		
CC	PD 05-DEC-1995		
CC	PF 21-APR-1994 JP 1994082836		
CC	PR 21-APR-1993 JP 93P 94491, 07-MAR-1994 JP 94P 36065		
CC	PI SHIMAMURA TOSHIAKI, HAMURO JUNJI, NAKAZAWA HARUHI,		
CC	KANAYAMA YUKA,		
CC	PI SUGAMURA KAZUO, TAKESHITA TOSHICHI		
CC	PC C12P21/08, A61K39/395, A61K39/395, C12N1/21, C12N5/20,		
CC	C12N15/13, C12N15/06,		
CC	PC C12P21/08, C12R1:19), (C12P21/08, C12R1:91), (C12N1/21, C12R1:19);		
CC	Key Location/Qualifiers		
CC	FH		
CC	CC FH		
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CC	FT	/cell_type="hybridoma"	
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CC	Key Location/Qualifiers		
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Best Local	Similarity 78.8%;	Pred. No. 2,238-207;		
Matches	487; Conservative	0; Mismatches 166;	Indels 7;	Gaps 5

Db	1	ATGATATATTCGCGACACAGCTCTCCAGCCTCCTCATCTGTCATCTGTGGGAGAAACTGT-	59
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Db	60	CACATCTCATGTGGAGCAATGGGAATATTCACAAATATTTAGCATGGATACAGGAA	112
Oy	61	CACATCTACTCTGCAGGGCCACCCCAAGTGT--A-AGTTACTGCATCTGATTCAGCGAAA	117
Db	120	ACAGGGAAATCTCTCCTCAGCTCTGGTCTATATATGCAAAAACCTTAGCAGATGGTGGCC	179
Oy	118	GCCAGGATCTCTCCCCCAACCTTGGATTTATACCAACATCCAACTKCTTCTGGAGTCCC	177
Db	180	ATCAAGTTCAGTGGCAGTGGATGAGCAACAAATATTTCTCAAGATTCACAGCCTGCA	239
Oy	178	TGCTCGCTTCAGTGGCGGTGGGTGTGGGACCTCTTACTCTCTCCACAGTCAGCAGAGTGGa	237
Db	240	GCCTCAAGATTTTGGGATTTATTTACTGTGCACATTTTGGAGTACTCGGAGCGTTGG	299
Oy	238	GGCTGAAAGATCTGCTCCACTTATTTACTGCCACAGATGGAGTGTGAGCCACCACAGTTGG	297
Db	300	TGAGGGACCAAGCTGGAGCTCAAGCTCGAAGATCGAAGAAATCTCAGAGATCTGGCTCCGATCCAA	359
Oy	298	AGGGGGGTCCAAAGCTGGAAATATAAG--GTCTCA-CCCTGTGGTCTGTGTAATCTTGa	354
Db	360	AAGCAGCAGAGTCAAACCTCGAGAGAGTCTGACCTGAGCTGTGAAGCCTGGGGCTTAGT	419
Oy	355	AGGTAAAGGTGTGCAGCTGCAGGAGTCAAGGACCTGAGAGTGTGAAGCCTGGAGGTTCAAT	414
Db	420	GAAGATATCTTCGCAAGGTTCTGGTACTCAATTCAGTGGGCTACAGATGACGAGCGGGTGA	479
Oy	415	GAAATATCTTCGCAAGACTTGTGGTACTCAATTCAGTGGGCTACAGATGACGAGCGGGTGA	474
Db	480	GCAAAAGCCATGTAAAGAGCCTTGAAGTGGATGAGCGATTAATCTTACCAATGGTGTAC	539
Oy	475	GCAGAGCCATGGAAGAAGACCTTGAAGTGGATGGACTTAATCTTACCAATGGTGTATC	534
Db	540	TAGTACACACCAAGATTTCAAGGACACAGGCCAGCTTGACTGTAGATTAAGTCTTCAGCAC	599
Oy	535	TAACTACACACCAAGATTTCAAGGACACAGGCCACCACTTACGTACACAAAGTCTTCACACAC	594
Db	600	AGCCTACATGGAGCTCCACACCTCGAATCTGAGAGACTGTCAGATCTAATTAAGTGGCAG	659
Oy	595	AGCTTACATGGAGCTCTCTCACTGTACATCTTGAGAGACTCTGCAATCTTAATTAAGTGGCAG	654

Db	120	ACGGGAAATTCCTCTCAGCTCCGTCGTCATTAATGCAAAAACCTTACAGATGGTGCC	179
Oy	118	GCCAGGATCCCTCCCCABACCCTTGATTTATACCACTCCACCTKCTTCTGGATCCC	177
Db	180	ATCAAGGTTCAGTGGCAGGTGATCAGACACAATATCTCTCAAGATCAACAGCCGTCA	239
Oy	178	TGCTGCTTCAGTGGCGGTGGGTGGGACCTCTTACTCTCTCACATTCAGCAGAGTGA	237
Db	240	GCCGTGAATATTTTGGAGTTATCTACTGTCAACATTTTGGAGTACTCCGCGAGCTTCGG	239
Oy	238	GCGTGAATATCTGCGCACTTATTACTGCGACAGATGAGTGTGAGCCACCCACGTTCCG	297
Db	300	TGAGGGACCAAGCTGTGAGCTGCACCAAGTCGAAATCCTCAGAGATCTGGTCCGCAATCCA	359
Oy	298	AGGGGGGTCCAAAGCTGGAAATTAAG--GTTCAT--CCTGTGTTCTGTGAATCTTCTGA	354
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Oy	415	GAAGTATCTGCAAGACTTCTGTTACTATTCACACTGCGCACCATGAACCTGGGTGAA	474
Db	480	GCAAAAGCATGTAAGAAGCCTTGAGTGGATTGGACGTATTAATCTTACAAATGGTGTAC	539
Oy	475	GCAGGCGCATGGAAGAACCCTTGAGTGGATTGGACTTATTAATCTTACATGGTGTATAC	534
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Oy	535	TAATCTACAAACCAAGATTCAGAGGGCAAGGCCACATTACTGTAGACAAGTCGTCCAGCAC	594
Db	600	AGCTCAATGAGAGCTCCACAGACCTGCAATCTGAGAGATCTGCACTATTAATCTGTGCAAG	659
Oy	595	AGCCTCAATGAGAGCTCTCACTGATGCAATCTGAGAGACTCTGCACTATTAATCTGTGCAAG	654

LOCUS	131036	729 bp	DNA	PAT	20-DEC-1996
DEFINITION	Sequence 3 from patent US 5582826.				
ACCESSION	131036				
NID	g1821827				
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 729) Shimmura,T., Hamuro,J., Nakazawa,H., Kanayama,Y., Sugamura,K. and Takeshita,T.				
TITLE	Monoclonal antibodies which bind the gamma chain of human interleukin-2 receptor				
JOURNAL	Patent: US 5582826-A 3 10-DEC-1996;				
FEATURES	location/Qualifiers				
SOURCE	1..729				
BASE COUNT	199 a	169 c	182 g	179 t	
ORIGIN	/organism="unknown"				
Query Match	39.2%	Score 279;	DB 21;	Length 729;	
Best Local Similarity	73.8%;	Pred. No.2.23e-207;			
Matches 487; Conservative	0;	Mismatches 166;	Indels 7;	Gaps 5;	

	RESULT	10		RNA	ROD	06-AUG-1995
	LOCUS					
	DEFINITION		MmIGJ013	Mouse hypidroma 2d3 mRNA for immunoglobulin kappa light chain v region.	Kappa light chain V	
	ACCESSION		X58586 Y00794			
	NID		G51562			
	KEYWORDS		Ig kappa light chain; Ig variable region;	immunoglobulin. house mouse.		
	SOURCE		Mus musculus			
	ORGANISM		Eukaryotee; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murineae; Mus.			
REFERENCE	AUTHORS		Meek,K. Submitted (09-JAN-1989)			
JOURNAL	TITLE		Medical School, 5333 Harry Hines Blvd. Microbiology, Dallas Texas 75235 USA			
REFERENCE	AUTHORS		2 (bases 1 to 321) Meek K., Hasemann,C., Pollak,B., Alkan,S.S., Bratt,M., Slaoui,M., Urbahn,J. and Capra,J.D.			
TITLE	JOURNAL		Structural characterization of antidiotypic antibodies. Evidence that Ab2s are derived from the germline differently than Abs			
MEDLINE	JOURNAL		J. Exp. Med. 169 (2), 519-533 (1989)			
FEATURES			89094248 Location/Qualifiers			
SOURCE			1..321			

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Db	60	CACCATCAGATGTGCAGCAAGTGGGAATATTCACATATTATTACATGATACGCGAA	119
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Db	14 CCCACTCTCCAGCATCCTGTCGTGCATGCCAGGGGAGAAGT-CACATGACTTGCAAG 72	
Oy	17 CCCACTCTCCAGCATCCTGTCGTGCATGCCAGGGGAGAAGTACACATGACTTGCAAG 76	
Db	73 GCCAGCTCAGTGTAGTTAGTATGATGCATGCTGTATCAGCAGAAACCAGATCCGCCAATA 132	
Oy	77 GCCACCCCAAGTGAAGTATGATGCATGCTGTATCAGCAGAAACCAGATCCGCCAATA 136	
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Oy	137 CCTTGATTATACCACTCACATCCAACTGCTTGTGAGTCCCTGCTGCCTTCAGTGGCAGT 196	
Db	193 GGGTCTGGAGACCTCTACTCTCTCTCATCATCCAGCAAGAGGAGGCTGAGATGCTGCCACT 252	
Oy	197 GGGTCTGGAGACCTCTACTCTCTCTCATCATCCAGCAAGAGGAGGCTGAGATGCTGCCACT 256	
Db	253 TATTACTGCCACCATGTGAGTAGTAACCCCCCAAGTTGCGAGGGGGAGACCAAGTGGAAA 312	
Oy	257 TATTACTGCCACCATGTGAGTAGTAACCCCCCAAGTTGCGAGGGGGAGTCCAACTGGAAA 316	
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Oy	317 ATAAAA 322	
RESULT	11	
LOCUS	A36642	315 bp DNA
DEFINITION	Sequence 2 from Patent EP0585570.	PAT
ACCESSION	A36642	05-MAR-1997
NID	g2293945	
KEYWORDS	.	
SOURCE	house mouse. Mus musculus	
ORGANISM	Eukaryota; Euteleostomi; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus	
REFERENCE	1 (bases 1 to 315)	
AUTHORS	Seemann,G. and Bosslet,K.	
TITLE	Antigranulocyte antibody construct, preparation and use thereof	
JOURNAL	Patent: EP 0585570-A 2 09-MAR-1994; BEHRINGERWERKE AG (DE)	
COMMENT	Other publication JP 6205693 940726 Other publication CA 2101868 940206 Other publication AU 4441393 940210 Other publication AU 666029 960125 Other publication DE 4225853 940210.	
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source	1..315 /organism="Mus musculus" /db_xref="taxon:10090" /cell_type="hybridoma/myeloma"	

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Best Local Similarity	93.3%;	Pred. No. 1,40e-199;		
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Db	60	AATGACTTTCAGGGCCAGCTCAGTGAATTACATGACTGTGTACAGCAAGAACCCAGG	119	
Qy	64	AATGACTTTCAGGGCCAGCTCAGTGAATTACATGACTGTGTATCAGCAAGAACCCAGG	123	
Db	120	ATTCCTCCCAAAACCCGATTTATGCAATCCAAACCGCTTGTGAGTCCCTGCTCG	179	
Qy	124	ATTCCTCCCAAAACCCGATTTATGCAATCCAAACCGCTTGTGAGTCCCTGCTCG	183	
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Qy	184	CTTCAGTGGCAGTGGGTCTGGGACCTTCTACTCTCTCACAAATCATCAGAGTGAAGCTGA	243	
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Qy	244	AGATGCTGCCACTTATTACTGCCAGCAGTGGAGTAGTAACCCGCTCACGTTGGGAGGGG	303	
Db	300	GACCAAGCTGGAGAT 314		
Qy	304	GTCACAGCTGGAAAT 318		
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LOCUS				PAT 12-AUG-1997
DEFINITION	Sequence 3 from patent US 5645817.			
ACCESSION	151657			
NID	92472858			
KEYWORDS	.			
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	Unclassified.			
AUTHORS	1 (bases 1 to 315)			
TITLE	Seemann, G. and Bosslet, R.			
JOURNAL	Granulocyte-binding antibody constructs, their preparation and use			
FEATURES	Patent: US 5645817-A 3 08-JUL-1997;			
	Location/Qualifiers			
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BASE COUNT	72 a	92 c	80 g	71 t
ORIGIN				
Query Match	37.9%;	Score 270;	DB 21;	Length 315;
Best Local Similarity	93.3%;	Pred. No. 1,40e-199;		
Matches 294;	Conservative	1;	Mismatches 19;	Indels 1; Gaps 1;
Db	1	GACATTCAGCTGACCCAGTCTCCAGCAATCTGTCTGCATCTCCAGGGGAGAGGT-CAC	59	
Qy	4	GACCTGAGCTGACCCAGTCTCCAGCAATCTGTCTGCATCTCCAGGGGAGAGGTACAC	63	
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Qy	64	AATGACTTTCAGGGCCAGCTCAGTGAATTACATGACTGTGTATCAGCAAGAACCCAGG	123	
Db	120	ATTCCTCCCAAAACCCGATTTATGCAATCCAAACCGCTTGTGAGTCCCTGCTCG	179	
Qy	124	ATTCCTCCCAAAACCCGATTTATGCAATCCAAACCGCTTGTGAGTCCCTGCTCG	183	
Db	180	CTTCAGTGGCAGTGGGTCTGGGACCTTCTACTCTCTCACAAATCATCAGAGTGAAGCTGA	239	
Qy	184	CTTCAGTGGCAGTGGGTCTGGGACCTTCTACTCTCTCACAAATCATCAGAGTGAAGCTGA	243	
Db	240	AGATGCTGCCACTTATTACTGCCAGCAGTGGAGTAGTAACCCGCTCACGTTGGTCTCG	299	
Qy	244	AGATGCTGCCACTTATTACTGCCAGCAGTGGAGTAGTAACCCGCTCACGTTGGGAGGGG	303	
Db	300	GACCAAGCTGGAGAT 314		
Qy	304	GTCACAGCTGGAAAT 318		

QY	244	AGATCTGCACATTTAACTGCGACAGACAGTGGAGTGCTGATGCCACCAACCCAGCTTGCGAGGGGG	303
Db	300	GACCAAGCTGGAGAT	314
QY	304	GTCCAAGCTGGAAAT	318
RESULT	13		
LOCUS	S48339	312 bp	mRNA
DEFINITION	Ig V kappa -anti-idiotypic Fab [mice, mRNA Partial, 312 nt].		
ACCESSION	S48339		
NID	9257749		
KEYWORDS			
SOURCE	Mus sp.		
ORGANISM	Mus sp.		
REFERENCE	1 (bases 1 to 312)		
AUTHORS	Kasai,Y., Herlyn,D., Sperlagh,M., Maruyama,H., Matsushita,S. and Linenbach,A.J.		
TITLE	Molecular cloning of murine monoclonal anti-idiotypic Fab		
JOURNAL	J. Immunol. Methods 155 (1), 77-89 (1992)		
MEDLINE	93017981		
REMARK	GenBank staff at the National Library of Medicine created this entry [NCBI gidsb 118382] from the original journal article. This sequence comes from Fig. 5.		
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ORIGIN			68 t
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Best Local Similarity	93.9%;	Pred. No. 7.55e-198;	Length 312;
Matches 290; Conservative 1;	Mismatches 17;	Indels 1;	Gaps 1;
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QY	14	TGACCCAGTTCACACATCCGTGTCATCCACGAGGAGAGAGTACACATGACTGC	73
Db	64	AGGCGACCTCAAGTGTAGTTACATGCAGCTGTACACAGACAGACCAAGATCTCCCC	123
QY	74	AGGCGACCTCAAGTGTAGTTACATGCAGCTGTATACAGACAGACCAAGATCTCCCC	133
Db	124	AAACCTGGATTATGACACATCAACCTGGCTTGAGAGTCCCTGCTTCAGTGGC	183
QY	134	AAACCTGGATTATATACCAATCCCAACCTGKGGCTTGAGAGTCCCTGCTTCAGTGGC	193
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QY	194	GGTGGCTGGAGCTCTTACTCTCTCAACATACACAGTGGAGGCTGAAGATCTGCC	253
Db	244	ACTTATTACTGCACAGTGTAGTGTAGTACCATGAGATGGTGGAGGACCAAGCTG	303
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[illegible]

AC T17728; (first entry)
 DE 21-MAY-1996
 DT Anti-erbB2 scFv cDNA.
 KW Oncoprotein; erbB2; cell proliferation; tumour; cancer;
 KW Intracellular antibody homologue; single chain antibody; scFv;
 KW gene therapy; ds.
 OS Synthetic.
 PN M09607321-A1.
 PD 14-MAR-1996.
 PE 23-AUG-1995; U10740.
 PR 06-SEP-1994; US-301339.
 PR 06-JUN-1995; US-468252.
 PA (UABR-) UAB RES FOUND.
 PI Curriel DT, Deshane J;
 DR WPI; 96-171307/17.
 DR P-PSDB; R94020.
 PT Inhibition of proliferation or survival of, esp. malignant erbB2,
 PT cells - by introducing nucleic acid mol. encoding antibody homologue
 PT which is expressed and binds, pref. erbB2, protein intracellularly
 PS Claim 42; Page 29-30; 48pp; English.
 CC A nucleic acid comprises a first sequence encoding a signal peptide
 CC (R94019) linked to a second sequence (T17728) encoding a single
 CC chain Fv fragment (R94020) that binds a human erbB2 oncoprotein.
 CC The anti-erbB2 scFv portion is obtained by PCR using e23scFv
 CC plasmid as template. The signal peptide directs the scFv to the
 CC endoplasmic reticulum. The nucleic acid is incorporated into a
 CC plasmid or viral vector to facilitate expression of the scFv antibody
 CC homologue within e.g. an epithelial carcinoma cell. Intracellular
 CC expression of the homologue inhibits surface expression of erbB2 and
 CC thereby inhibits cell proliferation and cell survival and decreases
 CC tumorigenicity.
 SO Sequence 711 BP; 175 A; 183 C; 189 G; 164 T;
 Query Match 98.2%; Score 699; DB 18; Length 711;
 Best Local Similarity 99.3%; Pred. No. 0.00e+00;
 Matches 707; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

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 Db cacaatgactgcaggggcccacccaagtgtatgatactgactggtatcagcagaagcc 119
 QY 1 CACATATGACTTGCAGGGGCCACCCCAAGTGTAACTGATGCACTGATGCAAGAACCC 120
 Db 120 agaatctctcccaaaccttgattatcacacacacacacacacacacacacacacac 179
 QY 121 AGGATGCTCCCAAACTTGATTTATACCAATCCAACTKGGTCTGAGTCCCTGC 180
 Db 180 tgcgttcagtgagggtggtgtctggagaccttactctctcagcagcagagtgagagc 239
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 QY 301 GGGGTCCAAAGCTGGAATAAAGGTTTACTCTGTTCTGTTTGAATCTTGAAGTAA 360
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 QY 361 AGGTGTGAGTGCAGAGGACCTGAGAGTGTGAGAGCTGAGAGTTCAATGAAGAT 420
 Db 420 atctgcagaagctctggttacttacttaccagcagcagcagcagcagcagcagcagcag 479
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 Db 480 ccatggaagaagacttgatgagcttataatccttacaatggtgtactactaacta 539
 QY 481 CCATGGAAGAAGACTTGATGAGATGAGACTTATTAATCCTTAACAATGATGATTA 540

Db 540 caaccagaagtccaaggcgaagccacattactgtgagaaagtcgtccagacagccta 599
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 Db 660 taaggactgttactcagatctctggggggaagagcagcagcagcagcagcagcagc 711
 QY 661 TACGAGCTGTGACTGTGATGTGGGGCGCAGGAGCACCGTCACCGTCTCC 712

RESULT 4
 ID T91615 standard; cDNA to mRNA; 720 BP.
 AC T91615;
 DE 22-DEC-1997 (first entry)
 DE cDNA encoding an anti-gp130 antibody derived scFv.
 KW Single chain Fv; scFv; antibody; E. coli; anti-T3 antibody;
 KW anti-gp130 antibody; inclusion body; chaparotin; ds.
 OS Synthetic.
 PN J09220092-A.
 PD 26-AUG-1997.
 PE 15-FEB-1996; 027622.
 PR 15-FEB-1996; JP-027622.
 PA (TOYT) TOSOH CORP.
 DR WPI; 97-474306/44.
 DR P-PSDB; W25784.
 PT Producing single chain Fv antibody in Escherichia coli - by
 PT expression in an inclusion body, followed by protein folding or by
 PT co-expression with a chaparotin as a soluble fraction
 PS Claim 4; Page 6-7; 9pp; Japanese.
 CC The sequences given in T91614-15 encode single chain Fv (scFv)
 CC antibodies which are produced in E. coli. The scFVs are derived
 CC from an anti-T3 antibody or an anti-gp130 antibody and are produced
 CC either by: (1) expression as an inclusion body, followed by folding
 CC (i.e. by denaturation and solubilisation) or (2) expression as a
 CC soluble fraction by co-expression with chaparotin. Using the methods,
 CC scFv can be produced in E. coli, either in a soluble fraction or in
 CC inclusion bodies. Like the parent double chain antibodies, the scFv
 CC polypeptides are useful in immunological diagnosis or for separation
 CC and purification, but they lessen the side effects caused by antibody
 CC constant regions. The availability of scFv polypeptides contributes
 CC to fundamental research and development of diagnostic and therapeutic
 CC drugs.
 SO Sequence 720 BP; 169 A; 193 C; 190 G; 168 T;
 Query Match 57.6%; Score 410; DB 34; Length 720;
 Best Local Similarity 83.1%; Pred. No. 1.02e-272;
 Matches 537; Conservative 1; Mismatches 104; Indels 4; Gaps 3;

Db 9 gctaccacagctctccaacatgatatactgcatctccagggagaaggt-caccatgacct 67
 QY 12 GCTAACCAAGCTCTCCACATCTCTGTCTGATCTCCAGGGAGAAAGTTACATATGACTT 71
 Db 68 gcaatgctcagctcaagtgttacttccatgtatgtgtacacagcagaagcagagatctccc 127
 QY 72 GCAGGGCCACCCCAAGTGAATGATGACATGCACTGTATGACAGAACCCAGAGATCTCCC 131
 Db 128 ccaaacctgattatctcaacatcacaactggtcttcttgagttccctccctgcagctg 187
 QY 132 CCAAACTTGGATTATTAACCAATCCATCCATGCTTGTGAGTCCCTGCTTCAAGT 191
 Db 188 gcaatggtctcggagacacttactctcacaacacagcagcttgagagctggaatgctg 247
 QY 192 CGGTTGGGTCTGGGACCTCTTACTCTCTCACAGTCACAGTGAAGTGAAGATCTCTG 251
 Db 248 ccaatttactgcagcagtgagagtaactaaccgcctcagcttgcgtgtcgtggagcagaac 307
 QY 252 CCACTTATTAATGCGACAGAGTGTGATGCGACCACTGAGGAGGGGCTCAAGC 311
 Db 308 tcgagctcgggtgaggggtggtcggggtggtgtggtgtggtgtggtgtggtgtggtgtc 367

QY 312 TCGAATAAAGTTTACCTCTGTTCTGTAAATCTTGTGANGTAA--GGT-GTCC 368
Db 368 aatcgacgagctctgacccggaactgtgaaagccctgggcttcagtgaaataaccctgca 427
QY 369 AGCTGACGAGTCTGAGCACTGAGGTGTGAAGCCTGGAGGTTCAATGAGATATCTGCA 428
Db 428 aggttcaagatatacacttactctacacaaagagctgtgtgaagcagagctatgaa 487
QY 429 AGACTTGTGTTACTCATCTACCTGCGCACACCATGAACTGGGTGAACGACAGCATGAA 488
Db 488 agagccttgatgtgattggaataatactcacaagtggtgtatattactacaaccaa 547
QY 489 AGAAGCTTGAATGATGACTTATTAATCTTCAATGGGATGATACACTACACAGA 548
Db 548 agttcaagagcaagggccatattgactgtatgaatgctcccaagcagccctacatgagc 607
QY 549 AGTTCAGAGGCAAGCCACATTTACTGTAGCAAGTGTGCGACGACGACCATGAGAGC 608
Db 608 tccgcagcctgacatctgagagacctgacgtctattatgtgcaag 653
QY 609 TCCCTACTGTGACATCTGAGACTCTGACGTCTATTAATCTGTGCAAG 654

RESULT 5

AC 765007 standard: cDNA: 720 BP.
DE 05-JUN-1997 (first entry)
KW Single-chain anti-erbB2 antibody e21(Fv) cDNA.
KW Single chain antibody; variable region; light chain; heavy chain;
KW breast cancer; ovarian cancer; non-small cell lung carcinoma;
KW Immunodiagnosis; treatment; cytotoxic agent; erbB-2; ds.
OS Mus musculus.
FH Synthetic.
FT Key
FT mat.peptide Location/Qualifiers
FT 1..720
FT /*tag= a
FT /product= e21(Fv)
PN US5587458-A.
PD 24-DEC-1996.
PF 07-OCT-1991: 772270.
PR 07-OCT-1991: US-772270.
PR 30-JUN-1992: US-906555.
PR 14-MAY-1993: US-061092.
PA (ARON-) ARONEX PHARM INC.
PI Bird RE, Kaspzyk PG, King CR;
DR WPI: 97-064831/06.
DR P-PSDB: W15186.
PT Single chain antibodies specific for erbB-2 protein, gp185 - with
PT labels or cytotoxin, useful for detection and treatment of tumour
PT cells expressing this protein
PS Example 9: Columns 27-30: 28pp: English.
CC The present cDNA sequence codes for a claimed single-chain antibody,
CC designated e21(Fv), which binds to erbB-2. Monoclonal antibody e21
CC was generated by immunising mice with N/erbB-2 cells overexpressing
CC the gp185 protein, removing spleen cells and producing hybridomas
CC by standard techniques. Messenger RNA coding for the anti-erbB-2
CC monoclonal antibody was isolated and converted to cDNA. Regions
CC coding for the heavy- and light- chain variable regions were then
CC amplified by PCR and joined via a sequence encoding a peptide
CC linker. The resulting single-chain antibody is useful for in vitro
CC diagnosis of tumour cells which overexpress the erbB-2 gp185
CC marker, e.g. breast, ovarian and non-small cell lung carcinomas,
CC and, when coupled to a cytotoxic agent, to treat such tumours.
SQ Sequence 720 BP: 184 A; 178 C; 179 G; 179 T;

Query Match 52.7%; Score 375; DB 29; Length 720;

Best Local Similarity 79.3%; Pred. No. 4.34e-247;
Matches 511; Conservative 1; Mismatches 131; Indels 1; Gaps 1;

Db 2 tgcagctgaccagctctcagcaatcaltgtctcatctcaggggaaaagt-caccatg 60
QY 8 TGCAGCTGACCAGCTCCAGCAATCTGCTGCATCTCCAGGGAGACAGTACACATG 67

Db 61 accctgagtgccagcccaagtgtgaaataacatgcatgtgtatcaggaagaagtcacacc 120
QY 68 ACTTGAGGGCCGCCCAAGTGAATGATTACATGCTGTGATACAGAGAAGCCAGATCC 127
Db 121 tcccccaactctgggtttatgacacatccaactctgctctgagctccagctcttc 180
QY 128 TCCCCCAAACTTGGATTATTAACCATCAATCCAACTTGCCTTCTTGAGATCCCTGCTCCTTC 187
Db 181 agtggcagtggtgtctggaactctctctcagcatcagcagcattgagagctgaaat 240
QY 188 AGTGGCGGTGGTGGTGGAGCCTTACTCTCTCAGTGAAGCAGAGATGGAGGCTGAAGAT 247
Db 241 gctgcacattattatgttcatcagggagtggtaccattcaagctgtgcctcgaggaa 300
QY 248 GCTGCCACTTATTAACGCCAGCAGTGAAGTGTGAGCCGCCACGCTTCGAGGGGGTCC 307
Db 301 aagttggaataaagaagcttaccctcgatcgtgtgaatctctgaaatgaagtgtg 360
QY 308 AACCTGGAATTAAGAAGTTCTTACCTTGCTTGTGTAATCTTTCTAAGGTAAGGTGTG 367
Db 361 cagctgcagcagctctgggttgagctgtccgagaggggacctgaagtgtcttcg 420
QY 368 CAGCTCAGAGAGTCAAGACCTGAGTGTGAAGCCTGGAAGGTTCAATGAATATCTCG 427
Db 421 aaagctctgacttaacattaaagactattatccactgggtgaggaagagcctgaa 480
QY 428 AAGACTTGTGTTACTCATCTACCTGCGCACACCATGAACCTGGGTGAAGAGCCATGCA 487
Db 481 caggcctggaatggaatgtgatgtattcatccctgagaatggaatcgtatagcccg 540
QY 488 AAGAACCTTGAAGTGATTTGAGACTTATTAATCTTACAAATGGTATTAATCAACACG 547
Db 541 aaattccaggccaagggcagatatacagacacacatccctcaagcggcctacttcag 600
QY 548 AAGTTCAAGGCAAGGCCACATTTACTGTAAGCAAGTCGCGACGACCTACATGAGAG 607
Db 601 ctcaagagcctgacatctgagagacatgcggtctatattactgtgc 644
QY 608 CTCTCAGTCTGACATCTGAGACTCTGACGTCTATTAATCTGTGTC 651

RESULT 6

ID 055181 standard: cDNA: 720 BP.
AC 055181;
DE Sequence encoding the single chain anti-erbB2 antibody, Ab no.21.
KW Single chain anti-erbB1 antibody; cancer therapy; prevention;
KW monoclonal antibody; ss.
OS Synthetic.
FH Key
FT Location/Qualifiers
FT 1..171
FT /*tag= a
PN MO9400136-A.
PD 06-JAN-1994.
PF 21-OCT-1992: U08545.
PR 30-JUN-1992: US-906555.
PA (MOLE-) MOLECULAR ONCOLOGY INC.
PI Kaspzyk PG, King CR;
DR WPI: 94-025878/03.
DR P-PSDB: R45443.
PT Treatment of malignancies over-expressing ERB-12 - using at least
PT 2 monoclonal antibodies which recognise different epitopes on
PT gp185
PS Example: Fig 8: 37pp: English.
CC The source of human erbB-2 protein for the prodn. of antibodies no.
CC 23 and 21 (055180/R45442; 055181/R45443) is a NIH/3T3 cell
CC engineered to express the human erbB-2 protein on its surface (N/
CC erbB-2). Abs no. 21 and 23 are directed against the extracellular
CC domain of gp185 erbB-2. Nude mice manipulated to produce rapidly
CC growing tumours were used in a trial of the efficacy of the Abs. In
CC animals given a combination of the 2 Abs, tumours completely
SQ regressed after 11 days
SQ Sequence 720 BP: 184 A; 178 C; 179 G; 179 T;

Query Match	Best Local Similarity	Score	DB	Length
Matches 487; Conservative	73.8%;	279;	12;	729;
		Pred. No. 4.18e-177;		
		Mismatches 166; Indels 7; Gaps 5;		
PA (AJIN) AJINOMOTO KK.				
PI Hamura J., Kenayama Y, Nakazawa H, Shimamura T, Sugamura K;				
P1 Takeshita T;				
DR WPI: 94-325948/41.				
DR P-PSDB: R60781.				
PT Immunosuppressant polypeptide - has ability to block				
PT Interleukin-2 response				
PS Claim 18; Page 29; 37pp; English.				
CC Mab capable of binding to the gamma chain of the IL-2 receptor, and				
CC thus of blocking the IL-2 response, is produced by mouse hybridoma				
CC line GP-4 (FERM BP-4640). DNA encoding the variable region of				
CC this Mab was expressed in E. coli, yielding Fv(GP-4) with				
CC immunosuppressive activity.				
Sequence 729 BP; 199 A; 169 C; 182 G; 179 T;				
Db 1 atgatatttcgtctgacacagcttcacagctccctccatctgcatctgtggagaactgt- 59				
Qy 1 ATGGACCTCGACAGCTGACCACCTCTCCAGCAATCTTGTCGATCTCCAGGGGAAAGTA 60				
Db 60 caccctccatctgctgagcaagtgtggaaatccaaattatttagcattggtatcagcagaa 119				
Qy 61 CACATGTACTTGCAGAGGGCCACCCCAAGGT--A-AGTTACATGTCATCGTATCGCGAGAA 117				
Db 120 acaagaaatctctccctcgcctcgtgtcatalatgcaaaaaccttagcagatgtgtcc 179				
Qy 118 GCCAGATCTCTCCCAACCTTGATTTATACACATCCACTKCTTCTGTGAGTCCC 177				
Db 180 atcaaggttcagttgacgtgacaaagaacaalattctctcaagaatcaacagctgtca 239				
Qy 178 TGCTGCTTCAAGTGGCGGTGGGTGGGACCTTACTCTCTACAGTACAGACAGAGTGA 237				
Db 240 gctctgaagatttggagattattactctgtcaacatttttggagatctccgtggagttcgg 299				
Qy 238 GCGTGAATATCTGCGCACTTATTACTGCGACAGTGGAGTGTGTCGCCACCCACAGTTCGG 297				
Db 300 tggagggacacagctctggagctccaagtctgagaatctccagatctgtgtccagatcaa 359				
Qy 298 AGGGGGTCCCAAGCTCGGAATAAAG--GTTCCTA-CCTCTGCTTCTGTGAATCTTCTGA 354				
Db 350 aagcagcaggttcaactctgagaggtctgtgacactgtgacactgtgtgagacctgtgagc 419				
Qy 355 AGGTAAAGGTGTGCGAGCTGACAGGTGACGACCTGTGAGGTGTGAAGCTTGAGGTTCAAT 414				
Db 420 gaagatactctgcaagaccttctgttactcaatctactgtgctactaatgcaactgtgtgaa 479				
Qy 415 GAAGATATCTCGCAAGAGATTCTGTGTTACTCATCTACATGCGCCACACATGAACTGGGTGAA 474				
Db 480 gcaaaagccatgtaagagccttggatgtgattgagcagatataatccttaagaatgtgttac 539				
Qy 475 GCAGAGCCATGAAAGAAACCTTGTAGTGGATTGAGCTTATTAATCTTAAATGGTGTATAC 534				
Db 540 tagctacaaccagaattccaaggaacaaggccagcttgcactgtagataagctctcaaac 599				
Qy 535 TAACACACACAGAAAGTTCAAGGGCAGGCGCACATTACTGTAGACAAAGTGTGACACAC 594				
Db 600 agcctacaatgtagctccacagcctgtgaactctgaggaactctgagcttactattactgtgcaag 659				
Qy 595 AGCCTACATGTGAGAGCTCCCATCTGACATCTGAGAGACTCTGCATGCTATTACTGTGCAAG 654				

FH	Key	Location/Qualifiers
FT	cds	22..462 /*tag= a
FT		/product= 3H1 heavy chain variable region
PN		M09620277-A2.
PD		04-JUN-1996
PF		28-DEC-1995; U17103
PR		28-DEC-1994; US-365484.
PA		(KENT) UNIV KENTUCKY.
PI		Chatterjee M., Chatterjee SK, Foon KA, Kohler H;
DR		Wpi: 96-321850/32. P-RSDs: R98411.
PT		Recombinant monoclonal anti-idiotypic antibody 3H1 sequences - used
PR		to develop prods. for the detection and treatment of
CC		carcinoembryonic antigen-associated diseases, partic. cancers
PS		Claim 6; fig 2A; 12pp; English.
CC		A CDNA clone (T31541) codes for the heavy chain variable region
CC		(VH) (R98411) of 3H1, a murine monoclonal anti-idiotypic antibody
CC		that mimics a specific epitope of the 180,000 mol.wt.
CC		carcinoembryonic antigen (CEA) and which elicits an immune response
CC		in patients with advanced CEA-associated disease, e.g. colorectal
CC		cancer. It was obt. by PCR amplification of 3H1 hybridoma DNA
CC		(see also T31545-46). The isolated polynucleotide, and/or a
CC		polynucleotide (see also T31540) coding for the VL region (R98410)
CC		of 3H1 can be used to design probes and primers, in expression
CC		systems, and in pharmaceutical applns., including vaccines, gene
CC		therapy and genetic immunisation, partic. against cancer.
SQ		Sequence 462 BP; 106 A; 124 C; 117 G; 115 T;
Query Match	37.4%; Score 266; DB 21; Length 462:	
Best Local Similarity	90.0%; Pred. No. 1,13e+167;	
Matches 316; Conservative 0; Mismatches 32; Indels 3; Gaps 2		
Dd	82 gtccgcctgcaaacagctcgacactgagctgggtgaagcttgagcttcactgaagaattccc 141	
Oy	365 GTGCACTGTGCAGGACATCGACACTGAAGTGTTGAAGCTTGAGGTTCAATGAATATATCC 424	
Dd	142 tgcgagctcttggtttacctactactcctaccacatgaactggtgaaagcacagcatc 201	
Oy	425 TGCAAGACTTGTGGTATTACTATTCTACTGCGCACACATGAACTGGTGAACACAGCAT 484	
Dd	202 ggaagagccttgagtgggttggtggtgatataccttcctcagtggtgatactaacaagc 261	
Oy	485 GGAAAGAACCCTTGAGTGATTTGGACTTWTATATCCTTAACAATGGTGATATACTAACAC 544	
Dd	262 cagaatatcaaggccaagggccacttaactgttaaacaggttatccagaacagcctaatcy 321	
Oy	545 CAGAAGTTCAAGGGCCAAGGCCACATTTACTGTAAACAAGTGTGCACACAGCCTTAATG 604	
Dd	322 gagccccctcagctgcacatcctgagaactctgagcttatattactgtgcatnaccgcggt 381	
Oy	605 GAGTCCTCATGTGACATCTGAGAGACTCTCAAGTCTATTACTGTG-CA-AGCAGGGTT 661	
Dd	382 ccctactgtagcttcgatgatlctggggcgacaggaaccaagctacagctctcc 432	
Oy	662 ACGGACTGTGACTTCGATGATGTCGGGGCGCAGGAGCAACGGTCAACCGTCTCC 712	
RESULT	10	
ID	T99435 standard; cdna; 462 bp.	
AC	T99435.	
DT	27-APR-1998 (first entry)	
DE	Anti-idiotypic antibody 3H1 heavy chain variable region CDNA.	
KW	Anti-idiotypic antibody 3H1; carcinoembryonic antigen; CEA;	
RW	tumour-specific antigen; tumour; colorectal cancer; lung cancer;	
KX	adenocarcinoma; therapy; ss.	
OS	Mus musculus.	
FH	Key	Location/Qualifiers
FT	CDS	22..462 /*tag= a
FN		M09738725-A1.
PD		23-OCT-1997.
PE		11-APR-1997; U05953.

Query Match	37.4%	Score 266;	DB 38;	Length 462;
Best Local Similarity	90.0%;	Pred. No. 1,13e-167;		
Matches 316;	Conservative 0;	Mismatches 32;	Indels 3;	Gaps 2;
Db 82 gtccagctgcacaagctcgcagcctgagctgtgtaagcctgagcttaactgaagattcc 141				
Oy 365 GTCCAGCTGCGAGGATCGAGACTGAGGTGGTGAAGCTGGAGGTTGTAAGAAATATCC 424				
Db 142 tgcgaggtcttggttactactactactgcaccacacatgaactggtgtaagcagacat 201				
Oy 425 TGCAGAGTCTGTGGTACTATCATCTACGTGCCACACACATGAAGCTGGGGAAGACAGCCAT 484				
Db 202 ggaagaagccttgagtggtgtggcgtgattatcccttcagtggtgtaactaactacagc 261				
Oy 485 GGAAGAAGACTTGTGATGGATGGACTTGTATATCTTACATGGTGTATCACTACAC 544				
Db 262 cagaattcacaggcgaagccacattactgtaagcagtgatccacacagcctcatg 321				
Oy 545 CAGAAGTTCAGAGGCGAAGCCACATTTACTGTAAACAAGTGTCCACACAGCCTTAATG 604				
Db 322 gagctccctcagcttgacacctcgcagagactcgcagctcatctactgctgcatcccggtc 381				
Oy 605 GAGCTCCTCAGCTGACACTGTGAGAGACTCTGACTCTATTACTGTG-CA--AGAGGGTT 661				
Db 382 cccctactgtaactcgaatgctgtggtggcgcaggaagacacagctacacgctctcc 432				
Oy 662 ACGAGCTGTGACTTCGATGTCTGGGGCGCAGGACACAGGTCCACGCTCTCC 712				
RESULT 11				
ID T34542 standard; cDNA; 462 BP.				
AC T34542;				
DE 11-OCT-1996 (first entry)				
DT Monoclonal anti-idiotypic antibody 3H1 VH cDNA				
PM Anti-Idiotypic antibody; monoclonal antibody; CEA;				
KW Carcinoembryonic antigen; tumour-associated antigen; cancer;				
KM vaccine; immunotherapy; ss.				
OS Mus sp.				
Key Location/Qualifiers				
FT cds 22..462				
FT /**tag= a				
PN W09620219-A2.				
PD 04-JUL-1996.				
PF 28-DEC-1995; U17105.				
PR 28-DEC-1994; US-365484.				
PA (KENT) UNIV KENTUCKY.				
PI Chatterjee M. Chatterjee SK, Foon KA, Kohler H;				
DR WPI: 96-321809/32.				
DR P-PSDB: R99687.				

PT	Monoclonal anti-idiotypic antibody 3H1 - elicits an immune response
PT	to carcinoembryonic antigen
PS	Example 2; Fig 2A; 102pp; English.
CC	A cDNA clone (J34542) codes for the heavy chain variable region
CC	(R39687) of monoclonal anti-idiotypic antibody 3H1 (ATCC HB 12003).
CC	It was obt'd. by PCR amplification (see also T4543-44) of cDNA
CC	derived from 3H1 hybridoma cells. Anti-idiotypic antibody 3H1
CC	elicits a specific immune response to a unique epitope of
CC	carcinoembryonic antigen (CEA) that is not present on other
CC	members of the CEA family or on normal adult tissues. 3H1
CC	can be used as a vaccine to elicit immune responses in patients
CC	with advanced CEA-associated disease or, when labeled, to enhance
CC	tumour detection in imaging.
SQ	Sequence 462 BP; 106 A; 124 C; 117 G; 115 T.
Query Match	37.4%; Score 266; DB 22; Length 462;
Best Local Similarity	90.0%; Pred. No. 1,13e-167;
Matches	316; Conservative 0; Mismatches 32; Indels 3; Gaps 2
Db	82 gtcacatgcaacacgtctgcagcctgcagctggtgtaagcctgcagcttactgaagattcc 141
Qy	365 gtcgacagctgcagagactgcagacactgcagagctggtgaagcttgagattcattcc 424
Db	142 tgcgaggtcttggttactcaactcaactgcctcaaccatgaactggtgtgaagcagaccat 201
Qy	425 tgcgaagacttgcgttactcattctactgcgcacacacatgaactgcgggaacacagccat 484
Db	202 ggaagagccttgagttggttcggctggtatcacttccttcagtggtgtaactaactcagc 261
Qy	485 ggaaggaaccttgatgattgagattgagacttattatctttaaactggtgacttactaacac 544
Db	262 cagaattcaccggaagggccacacttaactcgtgtagacaggtcatccacacagcctaatc 321
Qy	545 cagagttcaaggcgcacagccacatttactgctagacaaagtcgtccagacagcctaatc 604
Db	322 gagctcctcagtcgcacatctgaggaactcgtgcagtctatcactgttgcattactccggt 381
Qy	605 gagctcctcagtcgcacatctgaggaactcgtgcagtctatcactgttgcactgtg 661
Db	382 cccatctggaactcgcagtctcgtggggcgcaggaagcagggcaccggtctcc 432
Qy	662 acggaactggaactcgcagtctcgtggggcgcaggaagcagggcaccggtctctcc 712
RESULT	12
ID	Q65630. standard; DNA; 384 BP.
AC	Q65630.
DT	01-FEB-1995 (first entry)
DE	Murine variable region light chain from 2B8.
KW	B cell lymphoma chimeric antibody; CD20; peripheral blood cells;
KW	cell lysis; ss.
OS	Mus musculus.
PN	MO9411026-A.
PD	26-MAY-1994.
PF	12-NOV-1993; U10953.
PR	13-NOV-1992; US-978891.
PR	03-NOV-1993; US-149099.
PA	(IDBC-) IDEC PHARM CORP.
PI	Anderson DR, Hanna N, Leonard JE, Newman RA, Rastetter WH;
PI	Reifme;
DR	WPI; 94-183162/22.
DR	P-PSBD; R55214.
PT	Treating B cell lymphoma with chimeric antibody - against CD20,
PT	causing rapid depletion of peripheral B cells, also new
PS	antibodies and hybridomas
PS	Disclosure; Fig 4; 101pp; English.
CC	The sequence is the murine variable region light chain derived from
CC	murine anti-CD20 monoclonal antibody 2B8.
CC	See also Q65629-35.
SQ	Sequence 384 BP; 92 A; 106 C; 92 G; 94 T;
Query Match	37.2%; Score 265; DB 11; Length 384;
Best Local Similarity	93.8%; Pred.No. 5.98e-167;

Matches	287;	Conservative	1;	Mismatches	17;	Indels	1;	Gaps	1
Db	80	cccgagcttcgacgaatcctgctctcattccaggaggagaagt-cacaatgacttcgagg	138						
Qy	17	CCGAGTCCGACGACATCTGTCTGCATCTCCAGGGGAGAAAGTACACAATGACTTTCAGG	76						
Db	139	gcccagctcaagtgtgaagtgtacatccactgaggttcaggagcaggagatcctcccca	198						
Qy	77	GCCACCCCAATGTGAAGTGTACATGCATCGTATATAGCAGAAACGAGATCTCCCCCAA	136						
Db	199	cccttgatltatgcacaatcccaactggtctcttgagtcctgtctccttcagtcgagct	258						
Qy	137	CCTTGGATTATACACATCCACACTKCTCTTGAGTCCCTGCTCCTTACAGTGGGGT	196						
Db	259	ggagcttgagacttcttactctctcaccatcagcagagtgagagctgaagatgctgcact	318						
Qy	197	GGGCTGGGACCTTCTACTCTCACAGTCAGCAGAGTGGAGGCTGAAGATGCTGCCACT	256						
Db	319	tattactccgagctgagctagctgaaccaccacgttcggaggaggagaccagctgaa	378						
Qy	257	TATTACTCCGACGAGTGGAGTGTATAGCCACCCACGTTTGGAGGGGGTCCAACTGGAA	316						
Db	379	atcaaa 384							
Qy	317	ATATAA 322							
RESULT 13									
ID	Q65629	standard; DNA; 9208 BP.							
AC	065629;								
DT	01-FEB-1995	(first entry)							
DE	Vector contg. TCAE 8 DNA.								
KW	B cell lymphoma chimeric antibody; CD20; peripheral blood cells;								
MM	cell lysis; ss.								
OS	Synthetic.								
PN	MO9411026-A.								
PD	26-MAY-1994.								
PF	12-NOV-1993; U10953.								
PR	13-NOV-1992; US-976891.								
PR	03-NOV-1993; US-149099.								
PA	(IDEC-) IDEC PHARM CORP.								
PI	Anderson DR, Hanna N, Leonard JE, Newman RA, Rastetter WH;								
PI	Refine:								
DR	WPI: 94-183162/22.								
PT	Treating B cell lymphoma with chimeric antibody - against CD20,								
PT	causing rapid depletion of peripheral B cells, also new								
PT	antibodies and hybridomas								
PS	Disclosure: Fig 3: 101pp: English.								
CC	The sequence shows a vector contg. TCAE8, a gene encoding a chimeric								
CC	anti-CD20 antibody for treatment of B cell lymphomas. TCAE8								
CC	contains 4 transcriptional cassettes, human Ig light and heavy chain								
CC	constant regions, dihydrofolate reductase, neomycin phosphotransferase								
CC	and murine variable regions. The vector can be used to produce								
CC	antibodies which cause depletion of peripheral blood B cells,								
CC	including those associated with lymphoma. They mediate complement-								
CC	dependent lysis and lyse target cells by antibody-dependent cellular								
CC	cytotoxicity.								
CC	See also 065629-35.								
SO	Sequence 9208 BP: 2237 A; 2399 C; 2388 G; 2182 T;								
Query Match 37.1%; Score 264; DB 11; Length 9208;									
Best Local Similarity 93.2%; Pred. No. 3,17e-166;									
Matches 288; Conservative 1; Mismatches 19; Indels 1; Gaps 1;									
Db	1057	cccgagcttcgagcgaatcctgtctcattccaggaggagaagt-cacaatgacttcgagg	1115						
Qy	17	CCGAGTCCGACGACATCTGTCTGCATCTCCAGGGGAGAAAGTACACAATGACTTTCAGG							

QY	137	CCTTGAGATTATACCAATCCAACTTCTTGAGTCCCTGCTCCCTTACATGCGCGGT	196
Db	1236	ggagctcggagctcttctacccctccatccatccagcagagtgagagctgaagatgctgcacc	1295
QY	197	GGGCTCGGACCTCTTACTCTCTCAGAGTAGCAGAGTGGAGCGCTGAAGATGCTGCCACT	256
Db	1236	tattactcgcagcagtggtactagtaaccaccacccagcttcggaggggagccaagctgaa	1355
QY	257	TATTACTCCAGCAGATGGAGTCTGAGCCACCACCTTCCGAGGGGGTCCAACTGGAA	316
Db	1356	atcaaacgt 1364	
QY	317	ATTAAGGT 325	
RESULT	14		
ID	T79900	standard; cDNA; 318 BP.	
AC	T79900		
DT	27-DEC-1997	(first entry)	
DE	Anti-Factor IX MAB chimeric light chain cDNA.		
KW	Thrombosis; therapy; Factor IX; anticoagulant; monoclonal antibody;		
KS	Chimeric antibody; antibody engineering; light chain; ss.		
OS	Chimeric Mus musculus.		
OS	Chimeric Homo sapiens.		
PN	Chimeric synthetic.		
PN	W09726010-A1.		
PD	24-JUL-1997.		
PF	17-JAN-1997; U00759.		
PR	24-OCT-1996; US-029119.		
PR	17-JAN-1996; US-010108.		
PA	(SMIK) SMITHKLINE BEECHAM CORP.		
PA	(DUVE) UNIV VERMONT & STATE AGRIC COLLEGE.		
PI	Blackburn MN, Church WR, Feinstein GZ, Gross MS;		
PI	Nichols AJ, Padlan EA, Patel AH, Sylvester DR;		
DR	WPI: 97-385117/35.		
DR	P-PSDB: W24532.		
PT	Inhibiting thrombosis with self-limiting antibody to coagulation		
PT	factor - avoids uncontrolled bleeding by providing only partial		
PT	inhibition		
PS	Example 7; Page 128; 150pp; English.		
CC	This cDNA sequence encodes a mouse-human chimeric antibody		
CC	light chain (W24532) in which the variable region is derived		
CC	from mouse anti-human factor IX monoclonal antibody BC2 cDNA (see		
CC	TF79899) and human sequences from the immunoglobulin RF-TS3/CL		
CC	framework. It was obtained by PCR amplification (see T79897-98)		
CC	of BC2 cDNA and insertion of the PCR product into pFHZhc 1-3 cDNA		
CC	(see T77374). Claimed anti-Factor IX chimeric antibodies are		
CC	useful in the treatment of thrombosis.		
SQ	Sequence 318 BP; 79 A; 91 C; 78 G; 70 T;		
Query Match	36.9%; Score 263; DB 34; Length 318;		
Best Local Similarity	93.5%; Pred. No. 1.68e-165;		
Matches	286; Conservative 1; Mismatches 18; Indels 1; Gaps 1		
Db	14	ccagctcgcagcaatcctgctcgtcatctccaggaggaaggt-cacaatgacttcagg	72
QY	17	CCCAgTCCAGCAATCTCTGCTGCTCATCTCCAGGGAGAGAGTACAAATGACTCTGCAGG	76
Db	73	gcacagctaaagtgtaaataattacatcatcatgtaaccagagaagccagagatccctcccaaa	137
QY	77	GCCACCCCAAGTGAAGATTACATCACTGGATGATCAGAGAAACGAGATCCTCCCCAAA	136
Db	133	ccctggattttgccaatcatcaactcgtcttcgtgaatccctgtctccttcaggagcagt	192
QY	137	CCTTGGATTATTACCAATCCAACTTCTTGAGTCCCTGCTCCCTTACATGCGCGGT	196
Db	193	ggagctcggagctcttactcctccatccatccagcagagtgagagctgaagatgctgcacc	252
QY	197	GGGCTCGGACCTCTTACTCTCTCAGAGTAGCAGAGTGGAGCGCTGAAGATGCTGCCACT	256
Db	253	tattactcgcagcagtggtagttataaccacagagcgttcgttcgtgaggcacacaagctgaa	312

QY	257	TATTACAGCCAGAGTGTAGCCACACCAGTTGGAGGGGGGTCCAGCTGGAA	316
Db	313	atcaaa	318
QY	317	ATAAAA	322

RESULT	15
ID	T77377 standard; cDNA; 321 BP.

Query Match	36.9%;	Score 263;	DB 34;	Length 321;
Best Local Similarity	93.5%;	Pred. No. 1.68e-165;		
Matches	286;	Conservative	1;	Mismatches 18;
			Indels	1;
			Gaps	1;

Qy		257 TATTTCTCCGACAGTGGAGTCGTAGCCCCACCACCGTTGGAGGGGGTGCAACTGGAA	316
Db	313 atcaaa	318	
Qy	317 ATAAAA	322	

Search completed: Sat Jan 9 12:38:18 1999
Job time : 122 secs.

LOCUS	AA569186	387 bp	mRNA	EST	09-SEP-1997
DEFINITION	mm00d10.s1 NCI-CCAP_Lip2 Homo sapiens cDNA clone IMAGE:1061683 similar to gb:L02325 IG HEAVY CHAIN PRECURSOR V-I REGION (HUMAN).; mRNA sequence.				
ACCESSION	AA569186				
NID	92342240				
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
REFERENCE	1 (bases 1 to 387)				
AUTHORS	NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap .				
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index				
JOURNAL	Unpublished (1997)				
COMMENT					

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA library Preparation: David B. Krizman, Ph.D.
cDNA library Arrived by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNLT at: www.bio.llnl.gov/dbip/image/image.html

Insert Length: 1722 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 284.
Location/Qualifiers

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/organism="Homo sapiens"
/note="Vector: pAMP10; mRNA made from liposarcoma, cDNA made by oligo-dt priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."
/db_xref="taxon:9606"
/clone_image="IMAGE:1061683"
/clone_lib="NCI_CGAP_L1p2"
/tissue_type="liposarcoma"
/lab_host="DH10B"
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      mRNA
BASE COUNT      89 a      95 c      118 g      85 t
ORIGIN

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Query Match	Similarity	15.48;	Score 110;	DB 9;	Length 387;
Best Local	Similarity 69.08;	Pos. No. 1,05e-182;			
Matches	200; Conservative	0;	Mismatches 90;	Indels	Gaps 0;
Db	98	GTCCACTGGTGCACAGCTCGGGGCTGTGGAGGAAGCCCTGGGGCCCTCATGTGAAGCTTCC	157		
QY	355	GTCCAGCTTCGACAGAGTCAAGACCTGAGTGGTGGAAAGCCCTGGAGGTTCAATGAAATATCC	424		
Db	158	TGTATGGCATCTGGATTCACCTCCACCAACTCCCATATCATGTGGGTGGACAGGCCCT	217		
QY	425	TGCAGACTTTCGGTTACTCATCTACTGSCCACCACCATTAACCTGGTGGAAAGCAGAGCCAT	484		
Db	218	GGGCAAGGCGTTGATGGGTGGAAATGATCAATTCTAGTATGTTATATAAGTAACGCA	277		
QY	485	GGAAGAACCTTGATGGATGGACTTATTATTCCTTAACATGGTATCTACTACATCAAC	544		
Db	278	CAGAAGTTCACAGGCGAGAGTCAACCATGACCAAGGACACCTCCACGACCACTCTATATG	337		
QY	545	CAGAAGTTCAAAGGCGAAGCCCACTTACTTATGACAAACATCGCTCCGACGACACCTTCATG	604		
Db	338	GAGCTTAGAGCGCTGAGATCTGAGAGACAGCGCGCTCTATTACTGTGCCAG	387		
QY	605	GAGCTCTTAGTCTGACATCTGAGGAGCTCTGGAGTCTATTACTGTGCCAG	654		

RESULT	6								
LOCUS	AA110291	345 bp	mRNA	EST	24-DEC-1997				
DEFINITION	v33a04.11 Barstead mouse irradiated colon MPRB7 Mus musculus cDNA								
	V-16 REGION (HUMAN): gb:J00560 mouse 1g kappa chain PRECURSOR								
ACCESSION	AA110291								
NID	92720209								
KEYWORDS	EST.								
SOURCE	house mouse.								
ORGANISM	Mus musculus								
	Eukaryote; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;								
	Rodentia; Sciurognathi; Muridae; Murinae; Mus.								
REFERENCE	1 (bases 1 to 345)								
AUTHORS	Marra,M., Hallier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gaisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Thelsting,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.								
TITLE	The Washo-HMNI Mouse EST Project								
JOURNAL	Unpublished (1996)								

Contact: Marra M/Mouse EST Project
WashU-HM1 Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:632678
Seq primer: -28mJ rev2 ET from Amersham
High quality sequence stop: 140.

	FEATURES	SOURCE
	Location/Qualifiers	
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	/strain="FVB/N"	
	/note="Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: EcoRI; Site_2: NotI; Tissue obtained from 8 week old mouse. Colon was harvested 72 hours after irradiation with 1400 Gys. 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTAGGAGCGCCGCCCTTTTTTTTTTTTTTTT T 3'] ; double-stranded cDNA was ligated to Eco RI adaptors (AATTGGATCCTtg), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library constructed by Bob Barstead." /db_xref="taxon:"10090" /clone="1166766" /clone_lib="Barstead mouse irradiated colon MPLRB7" /dev_stage="8 weeks" /lab_host="DH10B"	
BASE COUNT	95 a	81 t
ORIGIN	81 c	

Query Match	12.9%	Score 92:	DB 11:	Length 345;
Best Local Similarity	66.9%	Pred. No. 2,72e-142;		
Matches 206;	Conservative	1;	Mismatches 99;	Indels 3; Gaps 3;
Db	35 TGACCAGCTCCAAAATTCATGTCACATAGCTGGAGACAGGGT-CAGCGTCACCTGC	93		
QY	14 TGACCCAGTCTCCAGCATCTCTGTCTGATATCTCCAGGGAGAGAGGTACACATGACTTGC	73		
Db	94 AAGCCAGTCAGATGTGGGTACTATGACCTGGTATCAAGAGAAACAGGCAATCTC	153		
QY	74 AGGGCCACCCCAA-CTGTA-AGTTACATGCACTGGTATCACAGAAAGCAGATCCTCC	131		
Db	154 CTAGAGCACTATTACTCGCGCATCTCCGGGTACAGTGGAGTCCCTGATGCTTCACAG	213		
QY	132 CCAAACTCTGGATTATATCCACATCAACCTTCGCTTGAGAGTCCCTCTGCTTCACTG	191		

Db	214	GCAGGATGATTCGGGACAGATTTCACTCTACCATCATGACGATTCGGAGCTGGAAAGATTGG	273
Oy	192	GGGGTGGGCTTGGGACCTTCTTACTCTTCACAGTCAGCAGAGTGGAGGCTGGAAGATGCTG	251
Db	274	CAGATGATTTCTGTGACGAAATATAACAGCTTCCGTCACAGCTTGGAGGGGGACCAACG	333
Oy	252	CCACTATTACTGCGCAGAGTGAGTGGTGGAGCCACGCCAGCTTGGAGGGGGTCCAAAC	311
Db	334	TGGAAATATAA	344
Oy	312	TGGAAATATAA	322
RESULT	7		
LOCUS	AA18377	333 bp	mRNA
DEFINITION	EST20620	Spleen I Homo sapiens cDNA 5' end similar to similar to immunoglobulin kappa light chain, V region, anti-thyroglobulin (GB:X79786), mRNA sequence.	
ACCESSION	AA18377		
NID	g1970863		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryotes: mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae;		
REFERENCE	1 (bases 1 to 335)		
AUTHORS	Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Butt,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man'hai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fitzhugh,J.L., Geoghegan,N.S., Glodde,J.A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudak,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dinke,D., Feng,D.-F., Ferite,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Korak,D.L., Kunsch,C., Hung,J., Xu,C., Yu,G.L., Ruben,S.M., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.		
TITLE	Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence		
JOURNAL MEDLINE	Nature 377 (6547 Suppl), 3-174 (1995)		
COMMENT	96026280		
	Contact: Kerlavage, AR		
	Bioinformatics		
	The Institute for Genomic Research		
	9712 Medical Center Drive, Rockville, MD 20850 USA		
	Tel: 3018699056		
	Fax: 3018699423		
	Email: arkerlav@tigr.org		
	For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)		
	Seq primer: M3 Reverse.		
FEATURES	Location/Qualifiers		
SOURCE	1..335		
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BASE COUNT			
ORIGIN			

Query Match	12.1%	Score 86	DB 24	Length 335
Best Local Similarity	67.1%	Pred. No. 4,99e-129		
Matches 159	Conservative 1	Mismatches 77	Indels 0	Gaps 0
Db	36	AGCTTTTACATGGTATCAGCACAACACAGGTAAGCCCTTAACCTCTGATCATGNT	95	
Oy	92	AGTTACATGACATGCTATCAGCAGAGACAGATCTCCCAACCTTGATTTATAC	151	
Db	96	ACATCCACTTTCGCAAGTGGGGTCCCATCAAGTTCAAGTGCATCGATCTGGGACAGAT	155	
Oy	152	ACATCCACTTTCGCTTTCGAGAGTCCCTCGCTCATGAGTGGGGGTCTGGGACCTCT	211	
Db	156	TTCACTCTCACCATCAGAGAGTCTGCACCTGAAGTTTTCACACTTACTCTACGTAACAG	215	
Oy	212	TACTCTCTCAGATGATAGAGAGTGGAGGCTGAAGATGCTGCACCTTATTTACTGCCAGAG	271	
Db	216	AGTTCCATAGAGCCCTTGGACGTTCTGGCCAGAGGNCACAGTGGCATATCAACGACACT	272	
Oy	272	TGGAGTCTGATAGCCACCCACACGTTGGAGGGGGGTCCCAAGCTGGAATATAAGGTTCT	328	
RESULT	8			
LOCUS	AA300571	279 bp	mRNA	EST 18-APR-1997
DEFINITION	EST13661	Testis tumor Homo sapiens	CDNA 5' end similar to similar	
		to immunoglobulin mu heavy chain, VDJC regions (GB:M18512), mRNA		
sequence.				
ACCESSION	AA300571			
NID	g1953132			
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
	Eukaryotee; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
REFERENCE	1 (bases 1 to 279)			
AUTHORS	Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fullner,R.A., White,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,			
	Butt,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wal,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,			
	Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Georgagen,N.S., Glodde,A., Grehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,			
	Kelley,J.C., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,			
	Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Uterbeck,T.R., Weidman,J.F., Li,Y.,			
	Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dinke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,			
	He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Korak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H.,			
	Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,			
	Fraser,C.M. and Venter,J.C.			
TITLE	Initial assessment of human gene diversity and expression patterns			
JOURNAL	Nature			
MEDLINE	377 (6547 suppl), 3-174 (1995)			
COMMENT	96026280			
	Other-ESTs: THC166571			
	Contact: Kerlavage, AR			
	Bioinformatics			
	The Institute for Genomic Research			
	9712 Medical Center Drive, Rockville, MD 20850 USA			
	Tel: 3018699056			
	Fax: 3018699423			
	Email: arkerlavet@tigr.org			
	For clone availability, additional sequence and expression			
	information related to this EST, please check the TIGR Human Gene			
	Index (http://www.tigr.org/cgi-bin/tigr.html)			
	Seq primer: M13 Reverse			
FEATURES	Location/Qualifiers			
source	1..279			

STAINING

the Not I and Eco RI sites of a modified pT7T3 vector

```

/1ab_host=DH10B (ampicillin resistant)
<1: .>379

```

Contact: Venter, JC

	COMMENT	Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@wustl.wustl.edu High quality sequence stops: 362 Source: IMAGE Consortium, LNL This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
	FEATURES	location/Qualifiers
	SOURCE	1..488
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		/clone="161528"
BASE COUNT	99 a 130 c 128 g 127 t 4 others	
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Query Match	11.4%	Score 81; DB 16; Length 488;
Best Local Similarity	66.7%	Pred. No. 4,51e-118;
Matches	154; Conservative	1; Mismatches 76; Indels 0; Gaps 0;
Db	168 AGTATTGGATGGGTGCTCCTGCAGAACCCAGACAGCATCTCCACAGCTCCTCATGTCATTTTG	227
Oy	92 AGTTACTGTCACCTGTRTCAAGCAAGACCAGGATCTCTCCCCAAACCTTGCGATTATACC	151
Db	228 GCCTTCTAAGCGGCCCTCCGGGCTCCCTGCAGAGTTTCAGTGCATGATCAGCACAGAT	287
Oy	152 ACATCCAACCKKGGTTCTGGAGTCCCTGGCTCGCTTCAGTGGGGGTCTGGAGACCTCT	211
Db	288 TTTCACACTGAGAATCAGTAGAGTGGAGAGCTCAGAGATGTTGGCTTTTATTACTGCATGCAA	347
Oy	212 TACTCTCTCACAGTACACAGAGTGGAGGCTGAAGAAGTCTCCACTTATTACTGCCAGCAG	271
Db	348 ACTCTACAGACCCCGCTCACTTTGGCGGGAGGAGACCAAGTCAGATNCA	398
Oy	272 TGAGACTGTAAGCCACCACCCACGCTTGGAGGGGGGCTCCAACTGGAATATAA	322
RESULT	13	
LOCUS	AA300732	333 bp mRNA EST 18-Apr-1997
DEFINITION	EST13847 Testis tumor Homo sapiens cDNA 5' end similar to similar	
	to Immunoglobulin kappa light chain (GB:S49006), mRNA sequence.	
ACCESSION	AA300732	
NID	G1953300	
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
	Eukaryota; Eukaryotic; mitochondria eukaryotes; Metazoa; Chordata;	
	Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae;	
	Homo.	
REFERENCE	1 (bases 1 to 333)	
AUTHORS	Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bull,C.O., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fitchman,J.L., Geoghagen,N.S., Glodak,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Mammosos,S.M., Merrick,J.M., Moreno-Palacios,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudke,D.M., Shirley,R., Small,K.V., Spilgus,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke-D., Feng,D.-F., Fertie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C. Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl.), 3-174 (1995)	
JOURNAL	Nature 377 (6547 Suppl.)	3-174 (1995)

FEATURES	source
<p>96026280 Other_ESTS: THC87411 Contact: Kerlavage, AR Bioinformatics The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850 USA Tel: 3016699056 Fax: 3016699423 Email: arkerlav@tigr.org For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tsg/tg/tg.html) Seq primer: M13 Reverse</p>	<p>Location/Qualifiers 1. .333 /organism="Homo sapiens" /note="Organ: testis; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI" /db_xref="ATCC (Inhost): 192041" /db_xref="taxon:9606" /clone_id="Testis tumor" /sex="male" /dev_stage="adult" <1. .>333</p>
<p>BASE COUNT 81 a 85 c 80 g 82 t 5 others</p>	
<p>ORIGIN</p>	
<p>Query Match 11.2%; Score 80; DB 24; Length 333; Best Local Similarity 67.7%; Pred. No. 6,81e-116; Matches 149; Conservative 1; Mismatches 70; Indels 0; Gaps 0;</p>	
<p>Db 3 CTGTGATGACAGAAAGCAGGAGAAAGCCCTGAGCTCTGATCTATGCTGATCCAGTTT 62 </p>	
<p>Oy 103 CTGGTATGACAGAGAGAGCCAGATCCTCCCAACACTTGATTAACACATCCAACTT 162 </p>	
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<p>Oy 163 KCGTTCTGGAGTCCCTGCTCCCTTCAGTGGGGGTGGTCTGGACCTTACTCTCTCAC 222 </p>	
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<p>Oy 223 AGTCAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTCGTG 282 </p>	
<p>Db 183 CCCGTGACGTTCCGCCAAGGAGCCAAAGTGGAAATCAA 222 </p>	
<p>Oy 283 CCCACCACAGTTCGGAGGGGCTCCAAAGCTGGAATAAATA 322 </p>	
<p>RESULT 14 LOCUS AA301347 413 bp mRNA EST 18-Apr-1997 DEFINITION EST14279 Testis tumor Homo sapiens CDNA 5' end similar to similar to immunoglobulin kappa light chain, V region (GB:L01279), mRNA sequence.</p>	
<p>ACCESSION AA301347 NID g1953680 KEYWORDS EST. SOURCE human. ORGANISM Homo sapiens Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. 1 (bases 1 to 413) Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstein,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man'wal,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Ene,L.D., Fitzgerald,L.M., Fitzhugh,M.M., Fritchman,J.L., Geoghagen,N.S., Glodde,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.V., Sauder,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utepbach,T.R., Weidman,J.F., Li,Y., Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,</p>	

|||||
OY 181 TCGCTCACTGGCGGTGGCTCTGGGACCTCTACTCTCTACAGCTAGCAGAGTGGAGGC 240
Db 240 TGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTCTAGACCCACCAGCTTGGAGG 299
OY 241 TGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTCTAGACCCACCAGCTTGGAGG 300
Db 300 GGGGTCCAAAGCTGGAATAAA 320
OY 301 GGGGTCCAAAGCTGGAATAAA 321

RESULT 2
LOCUS S39590 711 bp SYN 10-FEB-1993
DEFINITION anti-erbB2 immunotoxin antigen binding region (mice, Other
ACCESSION S39590
NID 9251113
KEYWORDS
SOURCE Mus sp.
ORGANISM Mus sp.
REFERENCE 1 (bases 1 to 711)
AUTHORS Batra,J.K., Kasprzyk,P.G., Bird,R.E., Pastan,I. and King,C.R.
TITLE Recombinant anti-erbB2 immunotoxins containing Pseudomonas exotoxin
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89 (13), 5867-5871 (1992)
MEDLINE 9235198
REMARK Genbank staff at the National Library of Medicine created this
entry [NCBI g18547] from the original Journal article.
This sequence comes from fig. 1.
FEATURES
source location/Qualifiers
1..711
/organism="Mus sp."
/db_xref="taxon:10095"
1..711
/partial
/gene="anti-erbB2 immunotoxin antigen binding region"
CDS
1..711
/partial
/gene="anti-erbB2 immunotoxin antigen binding region"
/note="This sequence comes from fig. 1."
/codon_start=1
/db_xref="pid:9251114"
/translation="MDLDLTGSPALISLSPKRYMTTCRATPSVSYHMYQKPGSSP
KPIYTTNLSAGVAPARSGSGSTSELYRYEADEAATYVQOMRSPRTGGGS
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HGKNEWISGLINPYNGSDTNYNOKFKGKATFTVDSSTSYAYWELLSTSEDSAYYYCAR
RVTDMYEPYMWAGTITVYS"

BASE COUNT 175 a 182 c 190 g 164 t
ORIGIN

Query Match 97.8%; Score 314; DB 31; Length 711;
Best Local Similarity 99.4%; Pred. No. 6.19e-249;
Matches 319; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Db 240 TGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTCTAGACCCACCAGCTTGGAGG 299
OY 241 TGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTCTAGACCCACCAGCTTGGAGG 300
Db 300 GGGGTCCAAAGCTGGAATAAA 320
OY 301 GGGGTCCAAAGCTGGAATAAA 321

RESULT 3
LOCUS I51657 315 bp DNA PAT 12-AUG-1997
DEFINITION Sequence 3 from patent US 5645817.
ACCESSION I51657
NID 92472858
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 315)
AUTHORS Seemann,G. and Bosslet,K.
TITLE Granulocyte-binding antibody constructs, their preparation and use
JOURNAL Patent: US 5645817-A 3 08-JUL-1997;
FEATURES
source location/Qualifiers
1..315
/organism="unknown"

BASE COUNT 72 a 92 c 80 g 71 t
ORIGIN

Query Match 84.1%; Score 270; DB 21; Length 315;
Best Local Similarity 93.3%; Pred. No. 3.01e-209;
Matches 294; Conservative 1; Mismatches 19; Indels 1; Gaps 1;

Db 1 GACATTCAGCTGACCCAGCTCTCCAGCAATCCTGTCGATCTCCAGGGAGAGGT-CAC 59
OY 4 GACCTGCAGCTGACCCAGCTCTCCAGCAATCCTGTCGATCTCCAGGGAGAGGTACAC 63
Db 60 AATGACTTGACGGGCGACGCTCAAGTGAATTACATGACGTGACCAAGCAGAACCCAG 119
OY 64 AATGACTTGACGGGCGACCCCAAGTGAATTACATGACGTGATACAGCAAGAACCCAG 123
Db 120 ATCTTCCCCCAACCTGATTTATGACACATCCAACTGGCTCTGGAGTCCCTGCTCG 179
OY 124 ATCTTCCCCCAACCTGATTTATGACACATCCAACTGCTCTGGAGTCCCTGCTCG 183
Db 180 CTTCAGTGGCAGTGGGTCTGGAGCTTACTCTCTCAATCATCAGAGTGGAGGCTGA 239
OY 184 CTTCAGTGGCAGTGGGTCTGGAGCTTACTCTCTCAAGTGGAGGAGGCTGA 243
Db 240 AGATCTGCCACTTATTCTGCGACAGTGGAGTGAATACCCGCTCAGCTCGGTCTGG 299
OY 244 AGATCTGCCACTTATTCTGCGACAGTGGAGTGGTGAATACCCGCTCAGCTCGGTCTGG 303
Db 300 GACCAAGCTGGAGAT 314
OY 304 GTCCAAGCTGGAAT 318

RESULT 4
LOCUS A36642 315 bp DNA PAT 05-MAR-1997
DEFINITION Sequence 2 from Patent EP0585570.
ACCESSION A36642
NID 92293945
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 315)
AUTHORS Seemann,G. and Bosslet,K.
TITLE Antigenulocyte antibody construct, preparation and use thereof
JOURNAL Patent: EP 0585570-A 2 09-MAR-1994;
BEHRINGWERKE AG (DE)

COMMENT	OTHER PUBLICATION	JP 6205693	940726
OTHER PUBLICATION	CA 2101868	940206	
OTHER PUBLICATION	AU 4441393	940210	
OTHER PUBLICATION	AU 666029	960125	
OTHER PUBLICATION	DE 4225853	940210.	
FEATURES	Location/Qualifiers		
SOURCE	1. .315		
ORGANISM	"/organism="Mus musculus"		
DB	"/db_xref="taxon:10090"		
ORIGIN	"/cell_type="hybridoma/myeloma"		
BASE COUNT	72 a 72 c 80 g 71 t		
Query Match	84.1%; Score 270; DB 21; Length 315;		
Best Local Similarity	93.3%; Pred. No. 3,01e-209;		
Matches	294; Conservative 1; Mismatches 19; Indels 1; Gaps 1;		
DB	1 GACATTCAGCTGACCCAGCTTCGACGAACTCTGTCTGATCTCCAGGGGAAAGGT-CAC 59		
OY	4 GACCTGACAGCTGACCCAGCTTCGACGAACTCTGTCTGATCTCCAGGGGAAAGGT-CAC 63		
DB	60 AATGACTTCGAGGGGACCTCAAGTGAAGTTACATGACGACGTGTACGACGAGAACCCAGG 119		
OY	64 AATGACTTCGAGGGGACCCCAAGTGAAGTTACATGACGACGTGTACGACGAGAACCCAGG 123		
DB	120 ATCTCTCCCAACCCCTTGATTTATGCCACATCCCAACCTGGCTTCTGGAGTCCCTGCTCG 179		
OY	124 ATCTCTCCCAACCCCTTGATTTATGCCACATCCCAACCTGGCTTCTGGAGTCCCTGCTCG 183		
DB	180 CTTCGATGGCAGTGGGTGTGGGACCTCTTACTCTCTACATCATCATGAGGGAGGCTGA 239		
OY	184 CTTCGATGGCAGTGGGTGTGGGACCTCTTACTCTCTACATCATCATGAGGGAGGCTGA 243		
DB	240 AGATCTGCGCACTTATTACTCCGACGAGTGGAGTGAACCCGCTCACGTTCCGCTGCTG 299		
OY	244 AGATCTGCGCACTTATTACTCCGACGAGTGGAGTGAACCCGCTCACGTTCCGCTGCTG 303		
DB	300 GACCAAGCTGGAGAT 314		
OY	304 GTCCAAAGCTGGAAAT 318		
RESULT	5		
LOCUS	MMIG013 321 bp RNA		
DEFINITION	Mouse hybridoma 2d3 mRNA for immunoglobulin kappa light chain V region.		
ACCESSION	X58586 Y00794		
NTID	g51562		
KEYWORDS	Ig kappa light chain; Ig variable region; immunoglobulin.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sclerogonathii; Myomorphia; Muridae;		
AUTHORS	Murine; Mus.		
TITLE	1 (bases 1 to 321)		
JOURNAL	Week, K.		
REFERENCE	2 (bases 1 to 321)		
AUTHORS	Week, K., Haseman, C., Pollok, B., Alkan, S.S., Bralt, M., Slaoui, M.,		
TITLE	Urbain, J., and Capra, J.D.		
JOURNAL	Structural characterization of anti-idiotypic antibodies. Evidence		
FEATURES	that Ab2s are derived from the germ-line differently than Ab1s		
FEATURES	J Exp. Med. 169 (2), 519-533 (1989)		
SOURCE	89094248		
Location/Qualifiers			
1. .321			
/organism="Mus musculus"			
/strain="Balb/c"			
/db_xref="taxon:10090"			
/cell_line="Hybridoma 2D3-K"			

FEATURES	Source
BASE COUNT	78 a 92 c 80 g 71 t
ORIGIN	LEIRR
gene	/gene="IG kappa light chain"
CDS	<1..321 /note="variable region"
mrna	/product="IG kappa light chain"
	<1..321 /gene="IG kappa light chain"
	/note="variable region"
	/evidence="experimental"
	1..321 /gene="IG kappa light chain"
	<1..321 /gene="IG kappa light chain"
	/note="variable region"
	/codon_start=1 /product="IG kappa light chain"
	/db_xref="PID:g938245"
	/translation="QIVLSOSPALLSAPGKVMTCRASSVSYNMYOOKPSSPK PWISATSNLASGVPARRSFGSGSGLTSLIRVEADPAATYCHQWMSNPPTFGGIRK LEIRR"
Query Match	84.1%; Score 270; DB 28; Length 321;
Best Local Similarity	94.8%; Pred No. 3 0le-209;
Matches	289; Conservative 1; Mismatches 14; Indels 1; Gaps 1;
Db	14 CCCAGCTCCGACCAATCCGTCTGTCATCTCCAGGGAGAGAGGT-CACATGACTTGCAGG 72
Qy	17 CCCAGCTCCGACCAATCCGTCTGTCATCTCCAGGGAGAGAGGTACACATGACTTGCAGG 76
Db	73 GCCAGCTCAAGTGAAGTTACATGCACAGTGTATCAGCAGAGACCGAGATCCTCCCAAAA 132
Qy	77 GCCACCCCAAGTGAAGTTACATGCACAGTGTATCAGCAGAGAACCGAGATCCTCCCAAAA 136
Db	133 CCCGTGATTTTCGCCACATCCCAACTGGGTTCTGAGATCCCGCTCGCTTCAGTGGCAGT 192
Qy	137 CCTTGATTTTATACACATCCCAACTGGGTTCTGAGATCCCGCTCGCTTCAGTGGCAGT 196
Db	193 GGGTCTGGGACCTCTTACTCTCTCAATTCAGCAGAGTGGAGGCTGAAGATGCTGCCACT 252
Qy	197 GGGTCTGGGACCTCTTACTCTCTCAAGTCAGCAGAGTGGAGGCTGAAGATGCTGCCACT 256
Db	253 TATTACTGCCACCAATGAGTAAACCCCAAGCTTCCGAGGGGGGACCAAGCTGGAA 312
Qy	257 TATTACTGCCACCAATGAGTAAACCCCAAGCTTCCGAGGGGGGACCAAGCTGGAA 316
Db	313 ATAAA 317
Qy	317 ATAAA 321
RESULT	6
LOCUS	S48339 312 bp mRNA ROD 14-JAN-1993
DEFINITION	IG V kappa -anti-idiotypic Fab [mice, mRNA Partial, 312 nt].
ACCESSION	S48339
NID	9257749
KEYWORDS	
SOURCE	Mus sp.
ORGANISM	Mus sp.
REFERENCE	1 (bases 1 to 312)
AUTHORS	Kasai, Y., Herlyn, D., Sperlagh, M., Maruyama, H., Matsushita, S. and Linnebach, A. J.
TITLE	Molecular cloning of murine monoclonal anti-idiotypic Fab
JOURNAL	J. Immunol. Methods 155 (1), 77-89 (1992)
MEDLINE	GenBank staff at the National Library of Medicine created this
REMARK	entry [NCBI gisbseq 118382] from the original journal article. This sequence comes from Fig. 5.
FEATURES	Location/Qualifiers
Source	1..312

gene
CDS
/organism="Mus sp."
/db_xref="taxon:10095"
1..312
/partial
/note="anti-idiotypic Fab"
/gene="Ig V<down>ekgr;</down>"
1..312
/partial
/gene="Ig V<kappa>"
/note="anti-idiotypic Fab; This sequence comes from F19."
5"
/codon_start=1
/db_xref="PID:9257750"
/translation="MTQSPALISPEEKVMTCRASSSVSYHMWQKPGSSPK
YATSNLASGVPARFSGSGSTSYSLTISRVAEDPATYYCOQMSNPNWTRGGCTKLE
IK"

BASE COUNT 76 a 88 c 80 g 68 t
ORIGIN

Query Match 83.2%; Score 267; DB 28; Length 312;
Best Local Similarity 93.8%; Pred. No. 1.51e-206;
Matches 289; Conservative 1; Mismatches 17; Indels 1; Gaps 1;

Db 5 TGACCCAGTCTCAGCAATCTGTGTCATCTCCAGGGGAGAAGT-CACATGACTTGC 63
|||
Oy 14 TGACCCAGTCTCAGCAATCTGTGTCATCTCCAGGGGAGAAGTACATGACTTGC 73
|||
Db 64 AGGCCAGCTCAAGTGTAGTATACATGACGTGACAGCAGAGCAGAGCTCTCCCC 123
|||
Oy 74 AGGCCAGCTCAAGTGTAGTATACATGACGTGATCAGCAGAGCAGAGCTCTCCCC 133
|||
Db 124 AACCCTGATTTATGCCATCCAACTGGCTTCGGAGTCCCTGCTTCAAGTGC 183
|||
Oy 134 AACCTGGATTATACCATCCAACTGGCTTCGGAGTCCCTGCTTCAAGTGC 193
|||
Db 184 AGTGGTGGAGCTCTACTCTCTCAGCATCAGCAGAGTGGAGCTGAGATGCTGC 243
|||
Oy 194 GGTGGTCTGGAGCTCTACTCTCTCAGCATCAGCAGAGTGGAGCTGAGATGCTGC 253
|||
Db 244 ACTATTACTGCCAGCAGTGTAGTATACCATGAGCTGGTGGAGGACCAAGCTG 303
|||
Oy 254 ACTATTACTGCCAGCAGTGTAGTATACCATGAGCTGGTGGAGGAGGCTCAAGCTG 313
|||
Db 304 GAATCA 311
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Oy 314 GAATCA 321
|||

RESULT 7 AF056217 318 bp mRNA ROD 13-APR-1998
LOCUS Mus musculus monoclonal antibody aH7:38 IgG1 light chain mRNA,
DEFINITION partial cds.
ACCESSION AF056217
NID 93044131
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 318)
AUTHORS Sandstrom,P., Johansson,A., Ullen,A., Behravan,G. and Stigbrand,T.
TITLE Differences in sequence and affinity between three monoclonal
anti-idiotypic antibodies against one anti-placental alkaline
phosphatase idiotypic antibody
UNPUBLISHED
JOURNAL 2 (bases 1 to 318)
REFERENCE Sandstrom,P., Johansson,A., Ullen,A., Behravan,G. and Stigbrand,T.
AUTHORS Direct Submission
TITLE Submitted (30-Mar-1998) Immunology, Umea University, Umea 90185,
JOURNAL Sweden
FEATURES Location/Qualifiers
source 1..318
/organism="Mus musculus"

CDS
/strain="balb/c"
/db_xref="taxon:10090"
/cell_line="hybridoma"
<1..318
/note="anti-idiotypic antibody against anti-placental
alkaline phosphatase antibody; variable region"
/codon_start=1
/product="monoclonal antibody aH7:38 IgG1 light chain"
/db_xref="PID:93044132"
/translation="DIQTSPALISPEEKVSMTCRASSSVSYHMWQKPGSSPK
PMIYATSNLASGVPRFSGSGSTSYSLTISRVAEDPATYYCOQMSNPNWTRGGCTK
LEIK"

BASE COUNT 74 a 91 c 81 g 72 t
ORIGIN

Query Match 83.2%; Score 267; DB 28; Length 318;
Best Local Similarity 92.5%; Pred. No. 1.51e-206;
Matches 294; Conservative 1; Mismatches 22; Indels 1; Gaps 1;

Db 1 GACATTCAGCTGACCCAGTCTCCAGCAATCTGTCTGATCTCCAGGGAGAAGT-CTC 59
|||
Oy 4 GACCTGACGCTGACCCAGTCTCCAGCAATCTGTCTGATCTCCAGGGAGAAGTACAC 63
|||
Db 60 AATGACTGACGGGACCTCAGTGTAGTATACATGACGTGACAGCAGAGCCAGG 119
|||
Oy 64 AATGACTGACGGGACCTCAGTGTAGTATACATGACGTGATGACAGAGCCAGG 123
|||
Db 120 ATCTCCCCCAACCTGTGATTTATGCCATCCAACTGGCTTCTGAGTCCCTGTTGC 179
|||
Oy 124 ATCTCCCCCAACCTGTGATTTATGACATCCAACTGGCTTCTGAGTCCCTGTTGC 183
|||
Db 180 CTTAGTGGAGTGGGTGGAGCTCTTACTCTCTCAATCAGCAGAGTGAAGCTGA 239
|||
Oy 184 CTTAGTGGAGTGGGTGGAGCTCTTACTCTCTCAATCAGCAGAGTGAAGCTGA 243
|||
Db 240 AGATCTGCCACTTATTCTGCGCAGAGTGGAGTGGATGCCGCTGCGTGGTGC 299
|||
Oy 244 AGATCTGCCACTTATTCTGCGCAGAGTGGAGTGGATGCCGCTGCGTGGTGC 303
|||
Db 300 GACCAAGCTGAGATCA 317
|||
Oy 304 GTCCAGCTGGAATCA 321
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RESULT 8 MUSIGRAR 1370 bp DNA ROD 05-FEB-1992
LOCUS Mouse Ig kappa active V-region from 702/3 cells.
DEFINITION K01641
ACCESSION K01641
NID G196460
KEYWORDS C-region; V-region; immunoglobulin light chain;
immunoglobulin-kappa.
SOURCE Mouse 702/3 cell DNA.
ORGANISM Mus musculus
Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Mus.
REFERENCE 1 (bases 1 to 1370)
AUTHORS Parslow,T.G., Blair,D.L., Murphy,W.J. and Granner,D.K.
TITLE Structure of the 5' ends of immunoglobulin genes: A novel conserved
sequence
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 81, 2650-2654 (1984)
MEDLINE 84194064
COMMENT Corrections to the sequence were sent by Dr. Richard E. Manroe and
Dr. Tristram G. Parslow on Dec. 9, 1991.
FEATURES Location/Qualifiers
source 1..1370
/organism="Mus musculus"
/db_xref="taxon:10090"
<776..824
/note="Ig kappa chain variable region"
/number=1
join(776..824,1003..1337)
/partial

	/note="Ig kappa chain variable region"
	/codon_start=1
	/db_xref="PID:g196461"
	/translation="MDFQVLFESFLILISAVIMSRGIVLSQSFAILLASBPGEKVTMT CRASSVSVMHYQQKPGSSSPKPWIAVTSMLASGVPARFSGGSTYSLTISRVEAE DAATYYCQOWSSNPRFTFGGKTLEIK" 825..1002
intron	/note="kappa cds: intron"
exon	1003..>1337 /note="Ig kappa chain variable region" /number=2 1338..>1369
intron	/note="kappa cds: intron j-c"
BASE COUNT	404 a 273 c 253 g 440 t
ORIGIN	
Query Match	82.9%; Score 266; DB 28; Length 1370;
Best Local Similarity 94.1%; Pred. No. 1,19e-205;	
Matches 287; Conservative 1; Mismatches 16; Indels 1; Gaps 1;	
Db 1033 CCCAGTCTCCAGCATTCCTGTCTGCATCTCCAGGGGAGAAGGT-CACATGACTTGCAAG 1091	
OY 17 CCCAGTCTCCAGCATTCCTGTCTGCATCTCCAAGGGAAGGTACACATGACTTGCAAG 76	
Db 1092 GCCAGCTCAAGTGTAGTAGTTACATGCATGCGTGTACAGCAAGAACCGAGATCCGCCCAA 1151	
OY 77 GCCACCACCAAGTGTAGTTACATGCATGCGTGTACAGCAAGAACCGAGATCCGCCCAA 136	
Db 1152 CCATGATTTATGCCACATCCAAACCTGGCTTGTGAGTCCCTGCTCGCTTCAGTGGCAGT 1211	
OY 137 CCTTGATTATATACACATCCAAACCTKGCTTGTGAGTCCCTGCTCGCTTCAGTGGCAGT 196	
Db 1212 GGGTGTGGACCTCTTAATCTCTCACATCAGACAAGTGGAGGCTGGAAGATCTCCACT 1271	
OY 197 GGGTGTGGACCTCTTAATCTCTCACAGTACAGACAAGTGGAGGCTGGAAGATCTCCACT 256	
Db 1272 TATTACTGCCAGCAGTGGAGTGTAAACCCAGGAGGTGGTGGAGGACCAAGCTGGAA 1331	
OY 257 TATTACTGCCAGCAGTGGAGTGTAGCCCCACCCAGCTTGTGGAGGGGGTCCAACTGGAA 316	
Db 1332 ATCAA 1336	
OY 317 ATAAA 321	
RESULT 9	
LOCUS MUSIGKVAZA 345 bp mRNA ROD 23-MAR-1994	
DEFINITION Mouse hybridoma Ig rearranged kappa-chain mRNA V-region, partial cds.	
ACCESSION M97864	
NID g197422	
KEYWORDS Immunoglobulin light chain; immunoglobulin-kappa; processed gene; variable region.	
SOURCE Mus musculus (strain BALB/c, sub-species domesticus) NS1-BALB/c fusion hybridoma CDNA to mRNA.	
ORGANISM Mus musculus	
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathii; Myomorpha; Muridae; Murinae; Mus. 1 (bases 1 to 345) Lohman,K.L., Kieber-Emmons,T. and Kennedy,R.C. Molecular characterization and structural modeling of immunoglobulin variable regions from murine monoclonal antibodies specific for hepatitis B virus surface antigen Mol. Immunol. 30 (14), 1295-1306 (1993)	
JOURNAL MEDLINE 94019421	
FEATURES	
source	Location/Qualifiers 1..345 /organism="Mus musculus" /db_xref="taxon:10090" 77 t
BASE COUNT	78 a 101 c 89 g 77 t
ORIGIN	

Query Match	82.6%	Score 265	DB 28	Length 345
Best Local Similarity	93.5%	Pred. No. 9,46e-205		
Matches 288	Conservative 1	Mismatches 18	Indels 1	Gaps 1

Db	7	CTCACCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAGAAAGT-CACAAATGACTTG	65
Oy	13	CTGACCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAGAAAGTACAAATGACTTG	72
Db	66	CAGGGCCAGTTCAAGTAGTTCATACACTGTGTACCAAGCAAGCCAGATCTCTCCC	125
Oy	73	CAGGGCCAGTTCAAGTAGTTCATACACTGTGTACCAAGCAAGCCAGATCTCTCCC	132
Db	126	CAAAACCCGAAATTAATGCAATCAACCTGGGCTTGGAGTCCCTGTGCTTCAGTG	185
Oy	133	CAAACTTGGATTAATTAACATCATCAACCTGGCTTGGAGTCCCTGTGCTTCAGTG	192
Db	186	CAGTGGGTCGGGAGACCTTCTACTCTCTCCACATAGCAGAGTAGAGCTGAAGATGCTGC	245
Oy	193	CGGTGGGTCGTGGAGACCTTCTACTCTCTCCACAGTACAGCAGATGGAGCTGAAGATGCTGC	252
Db	246	CACTTTCTACTGCCCAGCAGCTGGAGTAGTAACCCACCCAGTTCGGAGGGGGCTCCAGGCT	305
Oy	253	CACATTATTACTGCCAGCAGCTGGAGTCGTAGCCACCCAGCTTCGGAGGGGGCTCCAACT	312
Db	306	GGAAATTA 313	
Oy	313	GGAAATTA 320	

LOCUS	10	MUSIGKCN	403 bp	mRNA	ROD	26-MAR-1994
DEFINITION		Mouse Ig rearranged kappa-chain mRNA V55.				
ACCESSION		M17954				
NTD		g197015				
KEYWORDS		C-region; V-region; immunoglobulin light chain; immunoglobulin-kappa; processed gene.				
SOURCE		Mus musculus cDNA to mRNA.				
ORGANISM		Mus musculus				
		Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sclurognathi; Myomorphae; Muridae; Mus.				
REFERENCE		Li, A.Y., Robinson, R.R., Murray, E.D., Jr., Ledbetter, J.A., Hellstrom, I. and Hellstrom, K.E. Production of a mouse-human chimeric monoclonal antibody to CD20 with potent Fc-dependent biologic activity				
JOURNAL		J. Immunol. 139, 3521-3526 (1987)				
MEDLINE		88060445				
COMMENT		Draft entry and computer-readable sequence [1] kindly submitted by A.Y.Liu, 02-FEB-1987.				
FEATURES		Location/Qualifiers				
source		1..403				
		/organism="Mus musculus"				
		/db_xref="taxon:10090"				
		/cell_line="2H7"				
		20..>403				
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		/codon_start=1				
		/product="immunoglobulin kappa-chain"				
		/db_xref="PID:g466303"				
		/translation="MDROYQIFSLILASVIAIRGOIVLSQSPAILASPGKAVTWT				
		CRASSYSYMHYQOKRGSSEPKPIVAPSNLASSVPARFSGSSGTSYLTLSVLEAD				
		DAATYYCOQMSFNPTFGAGTKELK"				
		370..371				
		/note="V-region end/J-5-region start"				
		/organism="Mus musculus"				
BASE COUNT		100 a 112 c 93 g 98 t				
ORIGIN						

Query Match	81.6%	Score 262	DB 28	Length 403
Best Local Similarity	94.3%	Pred. No. 4,70e-202		
Matches 282	Conservative 1	Mismatches 15	Indels 1	Gaps 1

Db	99	CCAGCTCCAGCATCCTGCTCTGCATCTCCAGGGGAAGAAGT-CACAAAGACTTGGAG	157
Qy	17	CCCACTCCAGCAATCCTGCTCTGCATCTCCAGGGGAAGAAGTACAAATGACTTGGAGG	76
Db	158	GCCAGCTCAAGTGAAGTATACATGCACACTGATGATCCAGACAGAACCCAGGATCCTCCCAAA	217
Qy	77	GCCACCCCAAGTGAAGTATACATGCACACTGATGATGACAGACAGGATCCTCCCAAA	136
Db	218	CCAGGATTTATGCCCCATCCCAACCTGGCTCTGAGCCCTGCTCTCAGTGGAGT	277
Qy	137	CCTTGGATTTATACACATCCCAACTGCTTCTGAGTCCCTGCTCTCAGTGGAGGCT	136
Db	278	GGGCTTGGACCTTACTCTCTCACATCAGCAGAGTGAAGGCTGAAGATGCTGCCACT	337
Qy	197	GGGCTTGGACCTTACTCTCTCACATCAGCAGAGTGAAGGCTGAAGATGCTGCCACT	256
Db	338	TATTACTCCAGCAGTGGAGTTTAAACCAACCCAGCTGGTGGTGGAGCAACAGCTGA	396
Qy	257	TATTACTCCAGCAGTGGAGTTCGTAAGCCCAACCGTTTCGGAGGGGGGCTCCAAAGCTGA	315

LOCUS	11	109200	403 bp	PAT	14-NOV-1994
DEFINITION	Sequence 40 from Patent WO 8900999.				
ACCESSION	109200				
NID	9588127				
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 403)				
AUTHORS	ROBINSON, R.R., Liu, A.Y., Horwitz, A.H., Wall, R. and Better, M.				
TITLE	MODULAR ASSEMBLY OF ANTIBODY GENES, ANTIBODIES PREPARED THEREBY AND USE				
JOURNAL	Patent: WO 8900999-A 40 09-FEB-1989;				
FEATURES	Location/Qualifiers				
source	1..403				
BASE COUNT	100 a 113 c 92 g 98 t				
ORIGIN	"/organism="unknown"				
Query Match	81.6%; Score 262; DB 21; Length 403;				
Best Local Similarity	94.3%; Pred. No. 4,70e-202;				
Matches	282; Conservative 1; Mismatches 15; Indels 1; Gaps 1;				
Db	99 CCCAGCTCCGAGCAATCCTGTCGATCTCCAGGGGAGAAAGT-CACATGACTTGCAGG 157				
Oy	17 CCCAGCTCCGAGCAATCCTGTCGATCTCCAGGGGAGAAAGTACATATGACTTGCAGG 76				
Db	158 GCCAGCTCAAGTGTAGTACATGACGACTGTGTACCGACGACGAGAGCCAGAGTCTCCCCCAA 217				
Oy	77 GCCACCCCAAGTGTAGTACATGACGACTGTGTATCAGACGACGAGAGCCAGAGTCCCCCCAAA 136				
Db	218 CCCGAGATTATGCCCCCACTCCCACTGGCTTGGAGTCCCTGCTCGCTAGTGGCAGT 277				
Oy	137 CCTTGATTATACCCACATCCAACTCCCTCTTGGAGTCCCTGCTCGCTCAGTGGCGGT 196				
Db	278 GGGCTCTGGAGCTCTTACTCTCTCAATCAGACAGTGGAGGCTGAGATGCTCCACT 337				
Oy	197 GGGCTCTGGAGCTCTTACTCTCTCAAGTCAAGTCAAGAGTGGAGGCTGAAATGCTCCACT 256				
Db	338 TATTACTCCAGCAGTGGAGTTTAAACCACCCAGCAGTTCGGTGTGGAGACCAAGCTGGA 396				
Oy	257 TATTACTCCAGCAGTGGAGTGTGTAGCCCAACACAGCTTCGGAGGGGGGTCCAAAGCTGGA 315				
RESULT	12				
LOCUS	S76823	477 bp	mRNA	ROD	26-JUL-1995
DEFINITION	Ig V kappa -anti-sigma receptor Ig light chain [mice, hybridoma				
ACCESSION	S76823				
NID	9913971				
KEYWORDS					

SOURCE	Mus sp. hybridoma cell line 10G9.
ORGANISM	Mus sp. Eumarioteae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 477) Kobayashi,T., Togashi,S., Itoh,N. and Kumamishi,T. Molecular cloning of cDNAs for immunoglobulin variable regions of a monoclonal anti-idiotypic antibody specific for sigma receptors J. Neuroimmunol. 57 (1-2), 129-135 (1995)
AUTHORS	J. Neuroimmunol. 57 (1-2), 129-135 (1995)
TITLE	
JOURNAL	
MEDLINE	
REMARK	Genbank staff at the National Library of Medicine created this entry [NCBI gisbseq.163632] from the original journal article.
FEATURES	This sequence comes from Fig. 4. Location/Qualifiers

FEATURES	Location/Qualifiers
source	1..477 /organism="Mus sp." /db_xref="taxon:10095"
gene	52..477 /partial /note="anti-sigma receptor Ig light chain"
CDS	52..477 /partial /gene="Ig V κ ggr"
	/gene="Ig V κ kappa>" /note="monoclonal anti-idiotypic antibody specific for sigma receptors; This sequence comes from Fig. 4"
	/codon.start=1 /product="anti-sigma receptor Ig light chain" /db_xref="PID:g913972" /translation="MDFOVQIFSFLLISAVIISRQIVLSOSPALLSASPERKVTWT CRASSVSYSYIHWYQOKRSGSPKPMILATSNLAVGAPARFSGSGSTSYSLTISRMFAE DAATVYCOQWSRNLDTFGGGCTKLEIKRIMLHOLPSSHP"
BASE COUNT	125 a 128 c 106 g 118 t
ORIGIN	
Query Match	81.6%; Score 262; DB 28; Length 477; Best Local Similarity 93.4%; Pred. No. 4.70e-202; Matches 285; Conservative 1; Mismatches 18; Indels 1; Gaps 1;
Db	131 CCCAGTCTCCAGCAATCCTGTCGTCATCTCCAGGGGAGAAAGT-CACATGACTTTGCAGG 189
QY	17 CCCAGTCTCCAGCAATCCTGTCGTCATCTCCAGGGGAGAAAGTACACATGACTTTGCAGG 76
Db	190 GCCAGCTCAAGTGTAGTACATTCACTGCTGATCCAGCAGAGAACCCAGATCCTCCCAAA 249
QY	77 GCCACCCCAAGTGTAGTACATGACACGATGATCAGCAGAGAACCCAGATCCTCCCAAA 136
Db	250 CCCGGAATTTAGGCACATCCAACTGGCTTCTGGAGTCCCTGCTGCTTACGTGGCAGT 309
QY	137 CCTTGGAATTTATACACATCCAACTGGCTTCTGGAGTCCCTGCTGCTTACGTGGCAGT 196
Db	310 GGGTCTGGAGACTCTTACTCTCTCACATCCAGAAATGAGAGCTGAAGATGTCGCCACT 369
QY	197 GGGTCTGGAGACTCTTACTCTCTCACATCCAGAAATGAGAGCTGAAGATGTCGCCACT 256
Db	370 TATTACTGCCAGCAGTGGAGTGTGAACCTGTACAGCTTGCGGGGGGGAGCCAACTGGAA 429
QY	257 TATTACTGCCAGCAGTGGAGTGTGAACCTGTACAGCTTGCGGGGGGGAGCCAACTGGAA 316
Db	430 ATAAA 434
QY	317 ATAAA 321
RESULT	13
LOCUS	127490 321 bp DNA
DEFINITION	Sequence 4 from patent US 5565332.
ACCESSION	127490
NID	91818266
KEYWORDS	
SOURCE	Unknown.
ORGANISM	Unknown.
	PAT 16-OCT-1996

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 (TM)

Db	1	atggacgtcgagctgaccccaatcttcacgaacatctgtctgcatctccagggagaagtc-	59
Oy	1	atggacgtcgagctgaccccaatcttcacgaacatctgtctgcatctccagggagaagtc-	60
Db	60	caaatgactgtcagggccaccccaagtgtgaagttaactgtcactcgtgtatcagcagaacc	119
Oy	61	caaatgactgtcagggccaccccaagtgtgaagttaactgtcactcgtgtatcagcagaacc	120
Db	120	aggaatctcccccaaaccttgatattacacacatcccaaccctkgtctctgtagagtcctgc	179
Oy	121	aggaatctcccccaaaccttgatattacacacatcccaaccctkgtctctgtagagtcctgc	180
Db	180	tcgctcagtggtgcgttggtcttggtgaccttactcttcacagtcagcagatgtaggc	239
Oy	181	tcgctcagtggtgcgttggtcttggtgaccttactcttcacagtcagcagatgtaggc	240
Db	240	tgaagatctcccaacttactctgcacagcagtgtagtcgtatgaccacaccagttcgaag	299
Oy	241	tgaagatctcccaacttactctgcacagcagtgtagtcgtatgaccacaccagttcgaag	300
Db	300	ggggtcccaagctgtgaaataaa	320
Oy	301	ggggtcccaagctgtgaaataaa	321
RESULT	2		
ID	1	T65006 standard; cDNA; 711 BP.	
AC	1	T65006;	
DT	05-JUN-1997	(first entry)	
DE	Single-chain anti-erbB2 antibody e23(Fv) cDNA.		
KW	Single chain antibody; variable region; light chain; heavy chain;		
KW	breast cancer; ovarian cancer; non-small cell lung carcinoma;		
KW	immunodiagnosis; treatment; cytotoxic agent; erbB-2; ds.		
OS	Mus musculus.		
OS	Synthetic.		
FH	Key	Location/Qualifiers	
FT	mat_peptide	1..711	
FT		/*tag= a	
FT		/product= e23(Fv)	
PN	US5587458-A.		
PD	24-DEC-1996.		
PF	07-OCT-1991; US-772270.		
PR	07-OCT-1991; US-772270.		
PR	30-JUN-1992; US-906555.		
PR	14-MAY-1993; US-061092.		
PA	(ARON-) ARONEX PHARM INC.		
PI	Bird RE, Kasprzyk PG, King CR;		
DR	WPI: 97-064831/06.		
DR	P-PSDB: M5185.		
PT	Single chain antibodies specific for erbB-2 protein, gp185 - with		
PT	labels or cytotoxin, useful for detection and treatment of tumour		
PT	cells expressing this protein		
PS	Example 8: Columns 25-28; 28pp; English.		
CC	The present cDNA sequence codes for a claimed single-chain antibody,		
CC	designated e23(Fv), which binds to erbB-2. Monoclonal antibody e23		
CC	was generated by immunising mice with N/erbB-2 cells overexpressing		
CC	the gp185 protein, removing spleen cells and producing hybridomas		
CC	by standard techniques. Messenger RNA coding for the anti-erbB-2		
CC	monoclonal antibody was isolated and converted to cDNA. Regions		
CC	coding for the heavy- and light- chain variable regions were then		
CC	amplified by PCR and joined via a sequence encoding a peptide		
CC	linker. The resulting single-chain antibody is useful for in vitro		
CC	diagnosis of tumour cells which overexpress the erbB-2 gp185		
CC	marker, e.g. breast, ovarian and non-small cell lung carcinomas,		
CC	and, when coupled to a cytotoxic agent, to treat such tumours.		
SO	Sequence 711 BP; 175 A; 182 C; 189 G; 164 T;		
Query Match	97.8%;	Score 314;	DB 29; Length 711;
Best Local Similarity	99.7%;	Pred. No. 2.02e-204;	
Matches 320; Conservative	0;	Mismatches 0;	Indels 1; Gaps 1;
1	atggacgtcgagctgaccccaatcttcacgaacatctgtctgcatctccagggagaagtc-	59	

QY	1	ATGAGCTCGACAGTCAACCAAGTCTCTCCACCAATTCCTGTCTGCATCTCCAGGGAGAGGTA	60
Db	60	cacaatgactctcagggccaccccaagtgttaagtatactgacgcgtatacagagaagcc	119
QY	61	CACATATGACTTCAGAGGGCACCACCAAGTAAAGTTACATGCACATGRTACGCAAGAACCC	120
Db	120	aggatctctcccccacaaccttgattataccacatcccaacctkgtctcttgagttccctgc	179
QY	121	AGGATTCCTCCCCCAAACTTGATTTATACACATCCCAACTKCTCTTGAGATCCCTGC	180
Db	180	tgccttaagtgcggttggtctgagaccttactctcttcacaaatcagcagaatgagagc	239
QY	181	TGCGTTCAGTGGCGGTGGGTCTGGACCTCTTACTCTCTCCAGTCAAGCAAGTGGAGGC	240
Db	240	ttaaatgctgcacacttactctgcacagcagtgagtcgtatgcaccaccacgattcgaag	299
QY	241	TGAATATGCTGCGCACTTTTACTGCGACAGTGGAGTGTGATGCCACCCACGCTTCGAGG	300
Db	300	ggggtcccaagctggaataataa	320
QY	301	GGGTCCAAGCTGGAATAATAA	321
RESULT 3			
ID	T11728	standard; cDNA; 711 BP.	
AC	T11728;		
DT	21-MAY-1996	(first entry)	
DE	Anti-erbB2 scfv cDNA.		
KM	Oncoprotein; erbB2; cell proliferation; tumour; cancer;		
KW	Intracellular antibody homologue; single chain antibody; scfv;		
KW	gene therapy; ds.		
OS	Synthetic.		
PN	WO9607321-A1.		
PD	14-MAR-1996.		
PF	23-AUG-1995; U10740.		
PR	06-SEP-1994; US-301339.		
PR	06-JUN-1995; US-468252.		
PA	(UABR-) UAB RES FOUND.		
PI	Curtel DT, Deshane J;		
DR	PSDI: 96-171307/17.		
DR	P-PSDB: R94020.		
PT	Inhibition of proliferation or survival of, esp. malignant erbB2,		
PT	cells - by introducing nucleic acid mol. encoding antibody homologue		
PT	which is expressed and binds, pref. erbB2, protein intracellularly		
PS	Claim 42: Page 29-30; 48pp: English.		
CC	A nucleic acid comprises a first sequence encoding a signal peptide		
CC	(R94019) linked to a second sequence (T11728) encoding a single		
CC	chain Fv fragment (R94020) that binds a human erbB2 oncoprotein.		
CC	The anti-erbB2 scfv portion is obtained by PCR using e23scfv		
CC	plasmid as template. The signal peptide directs the scfv to the		
CC	endoplasmic reticulum. The nucleic acid is incorporated into a		
CC	plasmid or viral vector to facilitate expression of the scfv antibody		
CC	homologue within e.g. an epithelial carcinoma cell. Intracellular		
CC	expression of the homologue inhibits surface expression of erbB2 and		
CC	thereby inhibits cell proliferation and cell survival and decreases		
CC	tumorigenicity.		
CC	Query Match	97.2%; Score 312; DB 18; Length 711;	
CC	Best Local Similarity 99.1%; Pred. No. 5,83e-203;		
CC	Matches 318; Conservative 1; Mismatches 1; Indels 1; Gaps 1;		
Db	1	atggagctgcagagctgacccagctctcaggaacatctctctgcatctcctcaaggaggagaagt	59
QY	1	ATGGAGCTGCGAGCTGACCAAGTCTCCAGCAATCTGTCTGCATCTCCAGGGAGAAAGTA	60
Db	60	cacaatgacttcaggggcccacccaagtgttaagtatactgacgcgtatacagagaagcc	119
QY	61	CACATATGACTTCAGAGGGCACCACCAAGTAAAGTTACATGCACATGRTACGCAAGAACCC	120
Db	120	aggatctctcccccacaaccttgattataccacatcccaacctkgtctcttgagttccctgc	179
QY	121	AGGATTCCTCCCCCAAACTTGATTTATACACATCCCAACTKCTCTTGAGATCCCTGC	180
Db	180	tgccttaagtgcggttggtctgagaccttactctcttcacaaatcagcagaatgagagc	239
QY	181	TGCGTTCAGTGGCGGTGGGTCTGGACCTCTTACTCTCTCCAGTCAAGCAAGTGGAGGC	240
Db	240	ttaaatgctgcacacttactctgcacagcagtgagtcgtatgcaccaccacgattcgaag	299
QY	241	TGAATATGCTGCGCACTTTTACTGCGACAGTGGAGTGTGATGCCACCCACGCTTCGAGG	300
Db	300	ggggtcccaagctggaataataa	320
QY	301	GGGTCCAAGCTGGAATAATAA	321
QY	121	AGGATTCCTCCCCCAAACTTGATTTATACACATCCCAACTKCTCTTGAGATCCCTGC	180
QY	120	aggatctctcccccacaaccttgattataccacatcccaacctggtctctgagttccctgc	179
QY	121	AGGATTCCTCCCCCAAACTTGATTTATACACATCCCAACTKCTCTTGAGATCCCTGC	180

OS Mus musculus.
 PN W09726010-A1.
 PD 24-JUL-1997.
 PF 17-JAN-1997; U00759.
 PR 24-OCT-1996; US-029119.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PI (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.
 P1 Blackburn MN, Church WR, Feuerstein GZ, Gross MS;
 P1 Nicholas AJ, Padlan EA, Patel AH, Sylvester DR;
 DR WPI: 97-385117/35.
 DR P-PSDB: W24520.
 PT Inhibiting thrombosis with self-limiting antibody to coagulation factor - avoids uncontrolled bleeding by providing only partial inhibition
 PT Example 5: Page 64; 150pp; English.
 PS This cDNA sequence encodes the light chain variable region (see W24520) of mouse anti-human Factor IX monoclonal antibody BC2. CC Claimed humanised antibodies (see W24510-18) contain CDRs (see W24504-09) of BC2 heavy and light chains inserted into framework CC regions of selected human antibody sequences. They have self-limiting neutralising activity, and are useful as anticoagulant CC agents in treatment of thrombosis associated with myocardial CC infarction, unstable angina, atrial fibrillation, stroke, renal CC damage, pulmonary embolism, deep vein thrombosis, percutaneous CC transluminal coronary angioplasty, disseminated intravascular CC coagulation, sepsis, or artificial organs, shunts or prostheses CC (claimed). Also claimed are chimeric antibodies (see T79900), and CC Fab and Fab'2 fragments. The claimed antibodies do not cause CC uncontrolled bleeding (contrast heparin and warfarin) since they CC provide only partial inhibition of coagulation.
 SQ Sequence 321 BP; 78 A; 92 C; 79 G; 72 T;

Query Match 81.6%; Score 262; DB 34; Length 321;
 Best Local Similarity 93.4%; Pred. No. 1.52e-166;
 Matches 285; Conservative 1; Mismatches 18; Indels 1; Gaps 1;

DB 14 cccagctccagcaatccctgctgcatctccagggagaagt-cacatgactgcagg 72
 |||||||
 QY 17 CCCAGCTCCACCAATCCTGCTGCACTCCAGGAGAGATACATGATGCTTCAGG 76
 DB 73 gccagctcaagtgtaattacatgactggtaccagcagaacccagatccctcccaaa 132
 |||||||
 QY 77 GCCACCCCAAGTGAAGTATACATGCACTGCTGATCAGCAAGAACCCAGATCCCTCCCAAA 136
 DB 133 cccgtgattatgacacatccaaactggtcttgagtcctctgctgcttcagtgccagt 192
 |||||||
 QY 137 CCTTGATTTATACCAATCCCAACCTKGGCTTCTGAGATCCCTGCTCAGTGGCGGT 196
 DB 193 gggtctggagaccttactctctcacaatcagaagtggaagctggaagatgctgccaact 252
 |||||||
 QY 197 GGGTCTGGAGACCTCTTACTCTCTCAGAGTCACAGACAGATGAGGCTGAGATCTCCCACT 256
 DB 253 tattactgcagcagtgagatacctaaccacaggaagctcggtggagagcccaagctggaa 312
 |||||||
 QY 257 TATTACTGCCAGCATGTGAGTGTAGCCACCCACAGTTTCGAGGGGGGTCCAAAGCTGGA 316
 DB 313 atcaa 317
 |||||
 QY 317 ATAAA 321

RESULT 7
 ID T79899 standard; cDNA; 335 BP.
 AC T79899;
 DT 27-DEC-1997 (first entry)
 DE Anti-Factor IX Mab BC2 light chain PCR product.
 KW Thrombosis; therapy; Factor IX; anticoagulant; monoclonal antibody;
 KW Chimeric antibody; antibody engineering; light chain; ss.
 OS Chimeric Mus musculus.
 PN W09726010-A1.
 PD 24-JUL-1997.

PF 17-JAN-1997; U00759.
 PR 24-OCT-1996; US-029119.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PI (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.
 P1 Blackburn MN, Church WR, Feuerstein GZ, Gross MS;
 P1 Nicholas AJ, Padlan EA, Patel AH, Sylvester DR;
 DR WPI: 97-385117/35.
 DR P-PSDB: W24521.
 PT Inhibiting thrombosis with self-limiting antibody to coagulation factor - avoids uncontrolled bleeding by providing only partial inhibition
 PT Example 7: Page 126; 150pp; English.
 PS This cDNA sequence was obtained by PCR amplification (see T79897 CC and T79898) of the light chain variable region (see also T77377) CC of mouse anti-human factor IX monoclonal antibody BC2 cDNA. The CC amplification resulted in the addition of ScaI, NaeI ends to the CC VL region. The PCR product was ligated into ScaI, NaeI to produce a CC F9H2HC 1-3 (see T77374) and digested with ScaI, NaeI to produce a CC mouse-human chimeric light chain F9CHLC (see T79900, W24532). CC Claimed anti-Factor IX chimeric antibodies are useful in the CC treatment of thrombosis.
 SQ Sequence 335 BP; 80 A; 97 C; 85 G; 73 T;

Query Match 81.6%; Score 262; DB 34; Length 335;
 Best Local Similarity 93.4%; Pred. No. 1.52e-166;
 Matches 285; Conservative 1; Mismatches 18; Indels 1; Gaps 1;

DB 14 cccagctccagcaatccctgctgcatctccagggagaagt-cacatgactgcagg 72
 |||||||
 QY 17 CCCAGCTCCACCAATCCTGCTGCACTCCAGGAGAGATACATGATGCTTCAGG 76
 DB 73 gccagctcaagtgtaattacatgactggtaccagcagaacccagatccctcccaaa 132
 |||||||
 QY 77 GCCACCCCAAGTGAAGTATACATGCACTGCTGATCAGCAAGAACCCAGATCCCTCCCAAA 136
 DB 133 cccgtgattatgacacatccaaactggtcttgagtcctctgctgcttcagtgccagt 192
 |||||||
 QY 137 CCTTGATTTATACCAATCCCAACCTKGGCTTCTGAGATCCCTGCTCAGTGGCGGT 196
 DB 193 gggtctggagaccttactctctcacaatcagaagtggaagctggaagatgctgccaact 252
 |||||||
 QY 197 GGGTCTGGAGACCTCTTACTCTCTCAGAGTCACAGATGAGGCTGGAAGATGCTCCCACT 256
 DB 253 tattactgcagcagtgagatacctaaccacaggaagctcggtggagagcccaagctggaa 312
 |||||||
 QY 257 TATTACTGCCAGCATGTGAGTGTAGCCACCCACAGTTTCGAGGGGGGTCCAAAGCTGGA 316
 DB 313 atcaa 317
 |||||
 QY 317 ATAAA 321

RESULT 8
 ID N70972 standard; cDNA; 403 BP.
 AC N70972;
 DT 09-APR-1991 (first entry)
 DE 2H7 VL sequence in which the VK gene contains JK5 sequences.
 KW Chimeric antibody; Anti-cancer antibody; ss.
 FH Key
 FT cds
 FT 20...66
 FT /*tag- a
 FT /label=leader peptide
 FT 67...138
 FT /*tag- b
 FT /label=FR1
 FT 139...165
 FT /*tag- c
 FT /label=CDR1
 FT 166...210
 FT /*tag- d
 FT /label=FR2
 FT 211...231
 FT cds

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FT      /tag= e
FT      /label=CDR2
FT      232..327
FT      /tag= f
FT      /label=FR3
FT      328..354
FT      /tag= g
FT      /label=CDR3
FT      355..403
FT      /tag= h
FT      /label=FR4
FT      349..403
FT      /tag= i
FT      /label=Jk5
PN      MO8702671-A.
PD      07-MAY-1987.
PF      27-OCT-1986; U02269.
PR      01-NOV-1985; US-793980.
PA      (ITGE-) INT GENETIC ENG. INC.
PI      (ROBI/) ROBINSON R. R.
PI      Robinson RR, Liu AY, Horwitz AH, Wall R.
PI      WPI: 87-13604/19.
PI      P-PSDB: P70628.
PT      Prodn. of immunoglobulin chains and molecules - is by recombinant
PT      DNA procedures, with chimeric antibodies etc. related to cancer
PT      specific antigens.
PS      Example: Fig 22; 126pp; English.
CC      The patentors claim a chimeric antibody molecule comprising 2 light
CC      chains and 2 heavy chains, each comprising a constant human region
CC      and a variable non-human region. Coding sequences for the Ig chains
CC      are also claimed. The invention provides consensus sequences of
CC      light and heavy chain J regions useful in the design of
CC      oligonucleotides (UTS) for use as primers or probes for cloning
CC      immunoglobulinlight or heavy chain mRNAs or genes. Depending on the
CC      nature of design of a particular UIG, it may be capable of
CC      hybridizing to all Ig mRNAs or genes containing a single specific J
CC      sequence. UIG denotes universal immunoglobulin gene.
SQ      Sequence 403 BP; 100 A; 112 C; 93 G; 98 T;

Query Match      81.6%; Score 262; DB 2; Length 403;
Best Local Similarity 94.3%; Pred. No. 1.52e-166;
Matches 282; Conservative 1; Mismatches 15; Indels 1; Gaps 1;

Db      99 cccagctccagcaatcctgtctgcattccaggggagaaggt-cacaatgacttgcaag 157
QY      17 CCAGTCTCCAGCAATCCGTCTGCATCTCCAGGGGAGAGTACCAATGACTTGCAGG 76

Db      158 gccagctcaagttaagttacatgcatggtgtacagagagagcagagatctctcccaaa 217
QY      77 GCCACCCCAAGTTAAGTTATACATGCATGCTGTATCAGCAGAGCCAGATCTCCCCAAA 136

Db      218 cccgtgattatgcccatcaacactggtcttcgaggtccctctgcgtctcaatgagagat 277
QY      137 CCTTGATTTATACCATCATCAGCACTKGTCTTGAGAGTCCCTCTGCTTCATGTGGGGT 196

Db      278 gggctcggagacccctactctctccacaatcagcagagtgaggtcgaatgtgcgaact 337
QY      197 GGGTCTGGGACCTCTTACTCTCTCAGAGTCAAGAGTGAAGGCTGAAGTGTGCACACT 256

Db      338 tattactgcagcagtgaggttttaaccacccacaggttgctgtaggacacgtgaga 396
QY      257 TATTACTGCCAGCAGTGAAGTCTGTAGCCCAACCACTTTCGAGAGGGGGGTCCAAGCTGGA 315
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FT      /tag= a
FT      320..352
FT      /tag= b
FT      /note="JK5 region."
PN      WO8900999-A.
PD      9-FEB-1989.
PF      25-JUL-1988; 02514.
PR      24-JUL-1987; US-077528.
PA      (ITGE-) Int Genetic Eng. Inc.
PI      Robinson RR, Liu AY, Horwitz AH, Wall R, Better M.
PI      WPI: 89-061144/08.
PI      P-PSDB: P94778.
PT      Polynucleotide(s) encoding Immunoglobulin molecules -
PT      used for efficient prodn. of chimeric human or non-human or
PT      class switched antibodies.
PS      Disclosure; 7pp; English.
CC      Sequence, derived from M13 subclones of gene fragments, carries the
CC      variable region of chimeric immunoglobulin sequence. The antibodies are
CC      useful in passive immunisation avoiding negative reactions. They are
CC      also useful in assaying and in vitro imaging.
SQ      Sequence 403 BP; 100 A; 112 C; 93 G; 98 T;

Query Match      81.6%; Score 262; DB 1; Length 403;
Best Local Similarity 94.3%; Pred. No. 1.52e-166;
Matches 282; Conservative 1; Mismatches 15; Indels 1; Gaps 1;

Db      99 cccagctccagcaatcctgtctgcattccaggggagaaggt-cacaatgacttgcaag 157
QY      17 CCAGTCTCCAGCAATCCGTCTGCATCTCCAGGGGAGAGTACCAATGACTTGCAGG 76

Db      158 gccagctcaagttaagttacatgcatggtgtacagagagagcagagatctctcccaaa 217
QY      77 GCCACCCCAAGTTAAGTTATACATGCATGCTGTATCAGCAGAGCCAGATCTCCCCAAA 136

Db      218 cccgtgattatgcccatcaacactggtcttcgaggtccctctgcgtctcaatgagagat 277
QY      137 CCTTGATTTATACCATCATCAGCACTKGTCTTGAGAGTCCCTCTGCTTCATGTGGGGT 196

Db      278 gggctcggagacccctactctctccacaatcagcagagtgaggtcgaatgtgcgaact 337
QY      197 GGGTCTGGGACCTCTTACTCTCTCAGAGTCAAGAGTGAAGGCTGAAGTGTGCACACT 256

Db      338 tattactgcagcagtgaggttttaaccacccacaggttgctgtaggacacgtgaga 396
QY      257 TATTACTGCCAGCAGTGAAGTCTGTAGCCCAACCACTTTCGAGAGGGGGGTCCAAGCTGGA 315

RESULT 10
ID      T51043 standard; CDNA; 426 BP.
AC      T51043;
DT      06-AUG-1997 (first entry)
DE      Coding sequence for light chain variable region of 2H7.
KW      Precipitate lyase; signal sequence; Gram-negative bacterium; immunoglobulin;
KW      protein production; human; constant region; passive immunisation; toxin;
KW      serum sickness; anaphylaxis; sweetener; Chamaetia; cytoplasm; periplasm;
KW      myeloma cell; B-cell antigen; mouse; lung carcinoma; cancer;
OS      Mus musculus.
FH      Key      Location/Qualifiers
FT      cds      43..426
FT      /tag= a
FT      /product= light chain variable region of 2H7
PN      US5576195-A.
PD      19-NOV-1996.
PF      01-NOV-1985; 793980.
PR      01-NOV-1985; US-793980.
PR      27-OCT-1986; WO-002269.
PR      24-JUL-1987; US-077528.
PR      11-JAN-1988; US-142039.
PR      29-MAR-1990; US-501092.
PR      08-DEC-1992; US-987555.
PR      22-FEB-1993; US-020671.
PR      09-DEC-1994; US-357234.
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FT misc_feature 342..375
FT /tag= c
FT /note= "k5 sequence element
FT primer_bind 406..420
FT /tag= d
FT /note= "primer JKHindIII"
PN US5618920-A.
PD 08-APR-1997.
PR 01-NOV-1985; US-793980.
PR 01-NOV-1985; US-793980.
PR 27-OCT-1986; WO-002269.
PR 24-JUL-1987; US-077528.
PR 11-JAN-1988; US-142039.
PR 29-MAR-1990; US-501092.
PR 17-APR-1992; US-870404.
PR 29-APR-1994; US-235225.
PA (XOMA ) XOMA CORP.
PI Better M, Horwitz AH, Lei S, Liu AY, Robinson RR,
PI Wall R, Wilcox GL.
PI WPI: 97-225473/20.
DR P-PSDB: W16344.
PT Secretable immunoglobulin heavy and light chain fragments - capable
PT of assembling into chimeric antibodies, useful for e.g. passive
PT immunisation, diagnosis, etc
PT Example 4: Fig 22: 98pp: English.
CC A cDNA clone (T70869) codes for the light chain variable region
CC (W16344) of the 2H7 mouse monoclonal antibody, which recognises
CC human B-cell surface antigen Bp35. The sequence was isolated from
CC a 2H7 cell line cDNA library by PCR amplification. The 2H7 heavy
CC chain variable sequence (T60868) has also been isolated. The
CC sequences have been used to construct a human-mouse chimeric
CC antibody with specificity for the human B-cell antigen.
SQ Sequence 426 bp; 100 A; 135 C; 93 G; 98 T;

Query Match 81.6%; Score 262; DB 31; Length 426;
Best Local Similarity 94.3%; Pred. No. 1.52e-166;
Matches 282; Conservative 1; Mismatches 15; Indels 1; Gaps 1;

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QY 17 CCCAGCTCCAGCAATCCGTCTGCATCTCCAGGGAGAGATGACAAATGACTTGCAGG 76
Db 181 gccagctcaagttaagttacatgcactgttaccagcagagagccagatctctcccaaa 240
QY 77 GCCACCCCAAGTGTATGATGATGACATGCTGTATCAGCAGAGAGGATCTCCCAAAA 136
Db 241 cccctgattatgcccacccaacccctgcttgcagagtcctgcctcagtgagcag 300
QY 137 CCTTGATTTATACCAATCCAACTKGTCTTGAGAGTCCCTGCTTCATGAGCGGT 196
Db 301 gggctctggagaccttactctctcacaatcagcagagtgaggctgaagtctccact 360
QY 197 GGGCTCTGGAGCCCTTACTCTCTACAGTACAGAGAGTGGAGGCTGAAGATGCTGCAC 256
Db 361 tattactgcagcagagtgaggttttaacccccccacagctgctgctggaccacgtcga 419
QY 257 TATTACTGCCAGAGTGTAGTGTAGCCACCCACGTTGGAGGGGGGTCCAAAGTGA 315

RESULT 13
ID V03927 standard; cDNA. 426 bp.
AC V03927;
DE 01-JUN-1998 (first entry)
DT Mouse 2H7 antibody light chain variable region cDNA.
KW Mouse; murine; light chain; variable region;
KW immunoglobulin fragment production; Ig fragment production;
KW monoclonal antibody 2H7; human B-cell surface antigen; ss.
OS Mus sp.
FH key Location/Qualifiers
FT sig_peptide 43..108
FT /tag= a
FT mat_peptide 109..426
FT /tag= b
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PN US5693493-A.
PD 02-DEC-1997.
PR 25-MAR-1995; 450731.
PR 29-MAR-1990; US-501092.
PR 01-NOV-1985; US-793980.
PR 27-OCT-1986; WO-002269.
PR 24-JUL-1987; US-077528.
PR 11-JAN-1988; US-142039.
PR 08-DEC-1992; US-887555.
PR 18-AUG-1994; US-299085.
PR 25-MAY-1995; US-450731.
PA (XOMA ) XOMA CORP.
PI Better M, Horwitz AH, Lei S, Liu AY, Robinson RR,
PI Wall R, Wilcox GL.
PI WPI: 98-031749/03.
DR P-PSDB: W41071.
PT Production of chimeric antibody fragments - by culturing E. coli
PT transformed with dicistronic expression cassette
PS Example IV: Fig 22: 98pp: English.
CC The present sequence was used in the development of a novel method
CC for the production of an immunoglobulin (Ig) fragment capable of
CC binding an antigen. The method comprises culturing an E. coli host
CC that has been transformed with a nucleic acid molecule encoding the
CC Ig fragment, under conditions so that the Ig fragment is produced
CC and secreted. The nucleic acid molecule comprises DNA sequences
CC encoding: (a) pectate lyase secretion signal sequence operably
CC linked to a DNA sequence encoding at least the variable region of
CC an Ig Fd molecule; and (b) pectate lyase secretion signal sequence
CC operably linked to a DNA sequence encoding at least the variable
CC region of an Ig light chain, where (a) and (b) are operably linked
CC to a single prokaryotic promoter to form a dicistronic
CC transcription unit. The method is used to produce chimeric Fab
CC molecules, e.g. derived from murine monoclonal antibody 2H7 raised
CC against human B-cell surface antigen. The invention provides a
CC novel approach for producing genetically engineered antibodies of
CC desired variable region specificity and constant region
CC properties. The cloned Ig gene products can be produced by
CC expression in genetically engineered organisms. The application of
CC chemical gene synthesis, recombinant DNA cloning and production of
CC specific Ig chains in various organisms provides an effective
CC solution for the efficient large scale production of human
CC monoclonal antibodies. The invention also provides a solution to
CC the problem of class switching antibody molecules.
SQ Sequence 426 bp; 100 A; 135 C; 93 G; 98 T;

Query Match 81.6%; Score 262; DB 40; Length 426;
Best Local Similarity 94.3%; Pred. No. 1.52e-166;
Matches 282; Conservative 1; Mismatches 15; Indels 1; Gaps 1;

Db 122 cccagctccagcaatcctgtctgcatctccaggaggagaagt-cacaatgactgcagg 180
QY 17 CCCAGCTCCAGCAATCCGTCTGCATCTCCAGGGAGAGATGACAAATGACTTGCAGG 76
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QY 77 GCCACCCCAAGTGTATGATGATGACATGCTGTATCAGCAGAGAGGATCTCCCAAAA 136
Db 241 cccctgattatgcccacccaacccctgcttgcagagtcctgcctcagtgagcag 300
QY 137 CCTTGATTTATACCAATCCAACTKGTCTTGAGAGTCCCTGCTTCATGAGCGGT 196
Db 301 gggctctggagaccttactctctcacaatcagcagagtgaggctgaagtctccact 360
QY 197 GGGCTCTGGAGCCCTTACTCTCTACAGTACAGAGAGTGGAGGCTGAAGATGCTGCAC 256
Db 361 tattactgcagcagagtgaggttttaacccccccacagctgctgctggaccacgtcga 419
QY 257 TATTACTGCCAGAGTGTAGTGTAGCCACCCACGTTGGAGGGGGGTCCAAAGTGA 315

RESULT 14
ID V18558 standard; cDNA. 426 bp.
AC V18558;
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DT 05-JUN-1998 (first entry)
DE Mouse 2H7 antibody light chain variable region cDNA.
KW Mouse; murine; light chain; variable region;
KW immunoglobulin fragment production; Ig fragment production;
KW monoclonal antibody 2H7; human B-cell surface antigen; ss.
OS Mus sp.
FH Key location/Qualifiers
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FT mat_peptide /*tag= a
FT 109..426
FT /*tag= b
PN US5698435-A.
PD 16-DEC-1997.
PE 06-JUN-1995; 467140.
PR 29-MAR-1990; US-501092.
PR 01-NOV-1985; US-793980.
PR 27-OCT-1986; WO-002269.
PR 24-JUL-1987; US-077528.
PR 11-JAN-1988; US-142039.
PR 08-DEC-1992; US-987555.
PR 18-AUG-1994; US-299085.
PR 06-JUN-1995; US-467140.
PA (XOMA ) XOMA CORP.
PI Better M. Horwitz AH, Lei S, Liu AY, Robinson RR,
PI Wall R, Wilcox GL.
PI WPI: 98-051492/05.
DR P-PSDB: W47514.
PT DNA encoding secretable immunoglobulin fragments - comprising at
PS least the variable regions of light or heavy chains
PT Example IV: Fig 22: 98pp: English.
CC The present sequence was used in the development of a novel method
CC for the production of an immunoglobulin (Ig) fragment capable of
CC binding an antigen. The method comprises culturing an E. coli host
CC that has been transformed with a nucleic acid molecule encoding the
CC Ig fragment, under conditions so that the Ig fragment is produced
CC and secreted. The nucleic acid molecule comprises DNA sequences
CC encoding: (a) pectate lyase secretion signal sequence operably
CC linked to a DNA sequence encoding at least the variable region of
CC an Ig molecule; and (b) pectate lyase secretion signal sequence
CC operably linked to a DNA sequence encoding at least the variable
CC region of an Ig light chain, where (a) and (b) are operably linked
CC to a single prokaryotic promoter to form a dicistronic
CC transcription unit. The method is used to produce chimeric Fab
CC molecules, e.g. derived from murine monoclonal antibody 2H7 raised
CC against human B-cell surface antigen. The invention provides a
CC novel approach for producing genetically engineered antibodies of
CC desired variable region specificity and constant region
CC properties. The cloned Ig gene products can be produced by
CC expression in genetically engineered organisms. The application of
CC chemical gene synthesis, recombinant DNA cloning and production of
CC specific Ig chains in various organisms provides an effective
CC solution for the efficient large scale production of human
CC monoclonal antibodies. The invention also provides a solution to
CC the problem of class switching antibody molecules.
SQ Sequence 426 BP; 100 A; 135 C; 93 G; 98 T;

Query Match 81.6%; Score 262; DB 40; Length 426;
Best Local Similarity 94.3%; Pred. No. 1,52e-166;
Matches 282; Conservative 1; Mismatches 15; Indels 1; Gaps 1;

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QY 197 GGGTCTGGACCTCTTACTCTCAGCTCAGCAGAGTGAGGCTGAGAGTCTCCACT 256
DB 361 tactactccagcaagtggagtttaaccaccaccagctcgctgctggaccagctgga 419
QY 257 TATTACTGACACAGTGGAGTGTGAGCCACCCAGCTTCGGAGGGGGGTCCAGCTGGA 315

RESULT 15
ID V18594 standard; cDNA; 426 BP.
AC V18594;
DE 05-JUN-1998 (first entry)
DE Mouse 2H7 antibody light chain variable region cDNA.
KW Mouse; murine; light chain; variable region;
KW immunoglobulin fragment production; Ig fragment production;
KW monoclonal antibody 2H7; human B-cell surface antigen; ss.
OS Mus sp.
FH Key location/Qualifiers
FT sig_peptide 43.108
FT mat_peptide /*tag= a
FT 109..426
FT /*tag= b
PN US5698417-A.
PD 16-DEC-1997.
PE 06-JUN-1995; 466203.
PR 29-MAR-1990; US-501092.
PR 01-NOV-1985; US-793980.
PR 27-OCT-1986; WO-002269.
PR 24-JUL-1987; US-077528.
PR 11-JAN-1988; US-142039.
PR 08-DEC-1992; US-987555.
PR 18-AUG-1994; US-299085.
PR 25-MAY-1995; US-450731.
PR 06-JUN-1995; US-466203.
PA (XOMA ) XOMA CORP.
PI Better M. Horwitz AH, Lei S, Liu AY, Robinson RR,
PI Wall R, Wilcox GL.
PI WPI: 98-051487/05.
DR P-PSDB: W47521.
PT Production of recombinant immunoglobulin fragment - comprising Fd
PT molecule and light chain
PS Example IV: Fig 22: 98pp: English.
CC The present sequence was used in the development of a novel method
CC for the production of an immunoglobulin (Ig) fragment capable of
CC binding an antigen. The method comprises culturing an E. coli host
CC that has been transformed with a nucleic acid molecule encoding the
CC Ig fragment, under conditions so that the Ig fragment is produced
CC and secreted. The nucleic acid molecule comprises DNA sequences
CC encoding: (a) pectate lyase secretion signal sequence operably
CC linked to a DNA sequence encoding at least the variable region of
CC an Ig molecule; and (b) pectate lyase secretion signal sequence
CC operably linked to a DNA sequence encoding at least the variable
CC region of an Ig light chain, where (a) and (b) are operably linked
CC to a single prokaryotic promoter to form a dicistronic
CC transcription unit. The method is used to produce chimeric Fab
CC molecules, e.g. derived from murine monoclonal antibody 2H7 raised
CC against human B-cell surface antigen. The invention provides a
CC novel approach for producing genetically engineered antibodies of
CC desired variable region specificity and constant region
CC properties. The cloned Ig gene products can be produced by
CC expression in genetically engineered organisms. The application of
CC chemical gene synthesis, recombinant DNA cloning and production of
CC specific Ig chains in various organisms provides an effective
CC solution for the efficient large scale production of human
CC monoclonal antibodies. The invention also provides a solution to
CC the problem of class switching antibody molecules.
SQ Sequence 426 BP; 100 A; 135 C; 93 G; 98 T;

Query Match 81.6%; Score 262; DB 40; Length 426;
Best Local Similarity 94.3%; Pred. No. 1,52e-166;
Matches 282; Conservative 1; Mismatches 15; Indels 1; Gaps 1;

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Mon Jan 11 10:08:47 1999

US-08-704-178-1-02.rng

Page 9

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QY	137	CTGTGGATTATATACACATCCAACTTGCTTGTGAACTCCCTGCTCTTCACATGGGGT	196
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QY	257	TATTACTCCAGCATGTGAGTCGTAGCCCAACCCAGCTTCCGAGGGGGGTCCAAAGCTGA	315

Search completed: Sat Jan 9 14:32:20 1999
Job time : 65 secs.

MUSEUM

(TW)

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MPsrch_nu n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Sat Jan 9 13:35:31 1999, MasPar time 457.62 Seconds
1256.155 Million cell updates/sec

Tabular output not generated.

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Perfect Score: 321
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Comp: TACCTGACGTGACGTGAGT.....CCGAGTTCGACCTTATTT

Scoring table: TABLE default
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Searched: 2275026 seqs, 895388244 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

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10:gb_est14 11:gb_est15 12:gb_est16 13:gb_est17
14:gb_est18 15:gb_est19 16:gb_est20 17:gb_est21
18:gb_est22 19:gb_est23 20:gb_est24 21:gb_est25 22:gb_est26
23:gb_est27 24:gb_est28 25:gb_est29 26:gb_gss1 27:gb_gss2
28:gb_gss3 29:gb_gss4

Statistics: Mean 9.931; Variance 1.885; scale 5.267

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description	Pred. No.
1	232	72.3	396 11	AA691311 vs14f01.r1 Barstead mo	0.00e+00
2	179	55.8	344 9	AA592800 vo25g11.r1 Barstead mo	0.00e+00
3	91	28.3	345 11	AA710291 vt53a04.r1 Barstead mo	2.27e-131
4	84	26.2	335 24	AA318377 EST20620 Spleen I Homo	3.89e-117
5	81	25.2	393 16	T27593 EST100653 Homo sapiens	4.41e-111
6	80	24.9	488 16	H25625 y148g05.r1 Homo sapiens	4.53e-109
7	79	24.6	194 14	AA821173 yv34b07.r1 Stratagene	4.61e-107
8	79	24.6	333 24	AA300732 EST13847 Testis tumor	4.61e-107
9	79	24.6	413 24	AA301347 EST14279 Testis tumor	4.61e-107
10	78	24.3	253 24	AA295941 EST101165 Thymus IIT H	4.66e-105
11	78	24.3	370 24	AA295093 EST100400 Pancreas tum	4.66e-105
12	77	24.0	328 24	AA295311 EST100471 Pancreas tum	4.67e-103
13	76	23.7	210 16	R69482 yj83c03.r1 Homo sapien	4.64e-101

14	76	23.7	242 8	AA479857 zu35b05.r1 Soares ovar	4.64e-101
15	76	23.7	276 13	AA869306 vg50c10.r1 Barstead bo	4.64e-101
16	76	23.7	403 25	AA345486 EST51505 Gall bladder	4.64e-101
17	75	23.4	352 24	AA301261 EST14181 Testis tumor	4.57e-99
18	74	23.1	463 16	R69532 y182d09.r1 Homo sapien	4.46e-97
19	74	23.1	470 19	H62115 yu40h01.r1 Homo sapien	4.46e-97
20	73	22.7	345 25	AA335086 EST39457 Esophagus tum	4.31e-95
21	72	22.4	442 10	AA405415 zu56d02.r1 Soares ovar	4.13e-93
22	70	21.8	328 24	AA318628 EST20808 Spleen I Homo	3.67e-89
23	70	21.8	503 5	R28232 yh57e08.r1 Homo sapien	3.67e-89
24	69	21.5	339 11	AA710249 vt49e01.r1 Barstead mo	3.41e-87
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27	68	21.2	438 16	R64693 y122f09.r1 Homo sapien	3.14e-85
28	67	20.9	287 8	AA496610 zv38g06.r1 Soares ovar	2.85e-83
29	66	20.6	303 24	AA300891 EST14031 Testis tumor	2.56e-81
30	66	20.6	382 24	AA295786 EST100987 Pancreas tum	2.56e-81
31	66	20.6	398 10	AA423447 ve80a03.r1 Soares mus	2.56e-81
32	66	20.6	516 16	R67359 y142h11.r1 Homo sapien	2.56e-81
33	65	20.2	363 7	AA464313 zx78c12.r1 Soares ovar	2.28e-79
34	65	20.2	363 24	AA300651 EST13764 Testis tumor	2.28e-79
35	64	19.9	334 24	AA327254 EST30547 Colon I Homo	2.00e-77
36	64	19.9	390 16	HA5841 yp22b04.r1 Homo sapien	2.00e-77
37	64	19.9	397 5	R49771 y155c03.r1 Homo sapien	2.00e-77
38	63	19.6	261 5	R46878 y154h03.r1 Homo sapien	1.73e-75
39	63	19.6	357 25	AA361497 EST71040 T-cell lympho	1.73e-75
40	63	19.6	363 25	AA367405 EST78511 Pancreas tumo	1.73e-75
41	63	19.6	383 16	T29166 EST99871 Homo sapiens	1.73e-75
42	63	19.6	400 7	AA456778 zw37f11.r1 Soares ovar	1.73e-75
43	62	19.3	240 10	AA418046 zv33c09.r1 Soares ovar	1.48e-73
44	62	19.3	248 10	AA430449 zw20f11.r1 Soares ovar	1.48e-73
45	62	19.3	346 24	AA300582 EST13427 Testis tumor	1.48e-73

ALIGNMENTS

RESULT 1
LOCUS AA691311 396 bp mRNA
DEFINITION vs14f01.r1 Barstead mouse irradiated colon MPR47 Mus musculus cDNA
clone 1138201 5' similar to gb:x67211 M.musculus rearranged
immunoglobulin kappa light chain (MUSE);, mRNA sequence.

ACCESSION
NID AA691311
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE
AUTHORS Rodentia; Sciurognathu; Muridae; Murinae; Mus.
1 (bases 1 to 396)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisler,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Weisberg,B., Wyllie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.

TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT

CONTACT: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LBNL; contact the
IMAGE Consortium (info@image.lbnl.gov) for further information.
Seq primer: -28ml3 rev2 ET from Amersham.
Location/Qualifiers
1..396
/organism="Mus musculus"
/strain="FVB/N"
/note="Vector: pT73D-Pac (Pharmacia) with a modified

LOCUS	393 bp	EST	06-SEP-1995
DEFINITION	EST100653 Homo sapiens CDNA 5' end similar to immunoglobulin kappa light chain, V region (CB:L01279) (HT:30433).		
ACCESSION	J27593		
NID	9609691		
KEYWORDS	EST.		
SOURCE	human primer-M13 Reverse library-Human Pancreas.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostoma; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopteryyli; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homindae; Homo. 1 (bases 1 to 393)		
AUTHORS	Adams M.D., Kerlavage A.R., Fleischmann R.D., Fuldner R.A., Bult C.J., Lee N., Kirkness E.F., Weinstock K.G., Gocayne J.D., White O., Sutton G., Blake J.A., Brandon R.C., Chiu M.-W., Clayton R.A., Cline R.T., Cotton M.D., Earle-Hughes J., Fine L.D., Fitzgerald L.M., Fitzhugh W.M., Fritchman J.L., Geohagen N.S.M., Glodde A., Gnehm C.L., Hanna M.C., Hedblom E., Hinkle Jr P.S., Kelley J.M., Klinek K.M., Kelley J.C., Liu L.-I., Mamaros S.M., Merrick J.M., Moreno-Palauques R.F., McDonald L.A., Nguyen D.T., Pellegrino S.M., Phillips C.A., Ryder S.E., Scott J.L., Seidman D.M., Shirley R., Small K.V., Spriggs T.A., Utterback T.R., Weidman J.F., Li Y., Bednarek D.P., Cao L., Cepeda M.A., Coleman T.A., Collins E.-J., Dime D., Feng P., Ferlie A., Fischer C., Hastings G.A., He W.-W., Hu J.S., Greene J.M., Gruber J., Hudson P., Kim A., Kozak D.L., Kunsch C., Ji H., Li H., Weissner P.S., Olsen H., Raymond L., Wei Y.-F., Wang J., Xu C., Yu G.-L., Ruben S.M., Dillon P.J., Fannon M.R., Rosen C.A., Haseltine W.A., Fields C., Fraser C.M. and Venter J.C.		
TITLE	Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 52 Million Basepairs of CDNA Sequence		
JOURNAL	Unpublished (1995)		
COMMENT	Other-ESTs: THC24356		

	Query Match	Best Local Similarity	Matches	185: Conservative	Score 81; DB 16; Length 393; Pred. No. 4,41e-111; 1: Mismatches 81; Indels 4; Gaps 2;
Db	53	GACATCCAGATGAGCCAGTCCATCCCTCCCTGTCATCTGTAGAGAGACAGAGT-CAC 111			
QY	4	GACCTGAGGTGAGCCAGTCTCCAGCATCTGTCTCATCTCCAGGGGAGAAAGTTACAC 63			
Db	112	CTTCACTTGCCGGGGCAAGTCAAGACATTTAGCACACCTTTTAAATTTGGTATCAGCAGAAACC 171			
QY	64	AATGACTTGTGAGGGCCACCCCAAGTGTAATTTACATGTC---ACTGGTATCAGCAGAAAGCC 120			
Db	172	AGGGACAGCCCTTAAGTCTCTGATCTCTGCTGCATCCATTTTCGGAAGTGGGTCCCATC 231			
QY	121	AGGATCTCCCCCAAAACCTTGATTTATACCATCCCAACCTKAGCTTGTGAGTCCCTGC 180			
Db	232	AAGGTTACAGGGGCTGTGATCTGGGACAGATTTCACCTCACCATCAGCAGTGTGCACC 231			
QY	181	TGCCTTCAGTGGGGGTGGGTGTGGACCTTCTACTCTCTCAGTCAAGCAGCAGAGTGGAGGC 240			
Db	292	TGAAGATGTTGCAACTTACTACTGTCAACAG 322			
QY	241	TGAAGATGCTGCCACTTATTACTGCCAGCAG 271			

[illegible]

	<p>Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: estewartson.wustl.edu</p> <p>High quality sequence stops: 362 Source: IMAGE Consortium, LNL. This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.</p>					
FEATURES	Location/Qualifiers					
source	1..468					
BASE COUNT	99 a 130 c 128 g 127 t 4 others					
ORIGIN	/organism="Homo sapiens" /clone="161528"					
Query Match	24.9%; Score 80; DB 16; Length 488;					
Best Local Similarity	67.0%; Pred. No. 4,53e-109;					
Matches	152; Conservative 1; Mismatches 74; Indels 0; Gaps 0;					
Db	168	AGTTATTGGATTGGAACCTGCAGAAACCAGACAGTCTCCACAGCTCGATCTAATTG	227			
QY	92	AGTTACTTCACATGTGTATCAGCAAGAACCAGAGATCCCTCCCCAACCTTGATTTATACC	151			
Db	228	GCTTTAAGGGGCCCTCCGGGTCCTCGACAGATTAGTGGCAGTGGATGAGCACAGAT	287			
QY	152	ACATCCAACTKCTCTCTGGAGTCCCTGCTCGGTTAGTGGCGGTGGGACCTCT	211			
Db	288	TTTACACTGGAATAGTAGTGGAGGCTGAGAGTGTGGCTTTATTATCTCATGCAA	347			
QY	212	TACTCTCTCAGTCAAGCAGAGATGGAGGCTGAAGATGCTGCCACTATTATCTCCAGCAG	271			
Db	348	ACTCTACAGACCCCGCTCACTTTCGGCGGAGGAGACCAAGTGNAGAT	394			
QY	272	TGGAGTGTAGCCACCCACAGCTTGGAGGGGGGTCCAAGCTGGAAT	318			

LOCUS	AA921173	194 bp	mRNA	EST	20-APR-1998
DEFINITION	Y554b07.1	Stratagene mouse lung 937302	Mus musculus cDNA clone		
	1299253	5' similar to gb:X67211.M.musculus rearranged			
		immunoglobulin kappa light chain (MUSE);, mRNA sequence.			
ACCESSION	AA921173				
NID	93067952				
KEYWORDS	EST.				
SOURCE	house mouse.				
ORGANISM	Mus musculus				
	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;				
	Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 194)				
AUTHORS	Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisler,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theisinger,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.				
TITLE	The WashU-HHMI Mouse EST Project				
JOURNAL	Unpublished (1996)				
COMMENT	<p>Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LBNL; contact the IMGE Consortium (info@image.lbnl.gov) for further information. MG1:660301</p> <p>Trace considered overall poor quality Seq primer: -28m13 rev1 ET from Amersham High quality sequence stop: 1. Location/Qualifiers</p> <p>1..194 /organism="Mus musculus" /strain="C57BL/6 x CBA" /note="Organ: Lung; Vector: pBluescript SK-; Site:1: EcoRI; Site:2: XhoI; Cloned unidirectionally. Primer: Oligo dT. 6-8 month old female lung and 1.5 year old male lung were source of mRNA. Average insert size: 1.5 kb: Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGCGACGAGA 3' -3' adaptor sequence: 5' CTCGAGTTTATTTTATTTT 3'." /db_xref="taxon:10090" /clone.lib="Stratagene mouse lung 937302" /sex="female" /tissue_type="Lung" /dev_stage="6-8 month old" /lab_host="SOLR (kanamycin resistant)"</p>				
BASE COUNT	54 a	54 c	39 g	47 t	
ORIGIN					
Query Match	24.6%;	Score 79;	DB 14;	Length 194;	
Best Local Similarity	86.8%;	Pid. No. 4.61e-107;			
Matches	99;	Conservative	0;	Mismatches 14;	Indels 1;
Db	82	CCCAGCTCCACCATCATGCTCTAATCTCCACGGGAGGAAGT-CACCATGACCTCACT	140		
Oy	17	CCCCCTCTCCACCATCTCTGCTGCATCTCCACGGGAGGAGGATCACATGACTTCACAG	76		
Db	141	GCCATCTCAAGTATAGTAACTAGTACATGCTCTACACGACAGACGACGATCTCC	194		
Oy	77	GGCACCACCAAGTGAATGATACATGCACCTGTATCCACCAAGCAGATCTCTCC	130		
RESULT	8				
LOCUS	AA300732	333 bp	mRNA	EST	18-APR-1997
DEFINITION	EST11847	Testis tumor Homo sapiens cDNA 5' end similar to similar			
ACCESSION	AA300732				
NID	91953300				
KEYWORDS	EST.				

SOURCE	ORGANISM	REFERENCE	AUTHORS
human.	Homo sapiens	1 (bases 1 to 333)	Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Feldner,R.A., Bulc,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man'Wa,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodex,A., Gnehm,C.L., Hanna,M.C., Heblom,E., Hinkle,P.S., Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Uteback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J.J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungsh,C., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
JOURNAL MEDLINE		Initial assessment of human gene diversity and expression pattern based upon 83 million nucleotides of cDNA sequence	
COMMENT		Nature 377 (6547 Suppl.), 3-174 (1995)	
		96026280	
		Other ESTs: THC87411	
		Contact: Kerlavage, AR	
		Bioinformatics	
		The Institute for Genomic Research	
		9712 Medical Center Drive, Rockville, MD 20850 USA	
		Tel: 3018699056	
		Fax: 3018699423	
		Email: arkerlav@tigr.org	
		For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)	
		Seq primer: M13 Reverse.	
FEATURES			
SOURCE		Location/Qualifiers	
		1..333	
		/organism="Homo sapiens"	
		/note="Organ: testis; Vector: pBluescript SK-; Site-1: ECORI; Site-2: XhoI"	
		/db_xref="ATCC (inhost):192041"	
		/db_xref="taxon:9606"	
		/clone_lib="Testis tumor"	
		/sex="male"	
		/dev_stage="adult"	
		<1..333	
BASE COUNT	81 a 85 c 80 g 82 t 5 others		
ORIGIN			
Query Match	24.6%; Score 79; DB 24; Length 333;		
Best Local Similarity	67.6%; Pred. No. 4,61e-107;		
Matches 148; Conservative	1; Mismatches 107; Indels 0; Caps 0;		
Db	3 CTGGATATAGCAGAAACACAGGAAAGCCCTAAGCTTCTATGTATGCTCATCCAGTTT 62		
QY	103 CTGGATATAGCAGAAAGCCAGGATCCTCCCAACCTTGATATTATACCATCCCAACT 162		
Db	63 GCAAGTGGGGTCCCATCAAGTTCAGGCGAGGATGTGGGACAGATTTCACTCTCAC 122		
QY	163 KCGTCTTGAGATCCCTGCTCGCTTCATGCGGGGGGTCTGGGACCTCTTACTCTCTCAC 222		
Db	123 CATCAGCAGCCTGCAGCCCTGAAGATTTTGCACCTTACTATGTCAACAGGCTAACAATT 182		
QY	223 AGTCACAGAGTGGAGGCTGAAGATGCTGCACCTTATTACTGACAGAGTGGAGTGTAG 282		
Db	183 CCGGTGACGTTTGGGCCAAGGACCAAGGTGGAATCAA 221		
QY	283 CCCACCCAGTTCGAGGGGGGTCCAAAGCTGGAATATAA 321		

[illegible]

Db	197	AGGGAAGACCCCTAGACGTCGATGATGATGTCATCCATCCAGTTTGCAAGGCGGGCTCCCTTC	256
Oy	121	AGGATCTCTCCCCCAACCTTGAGATTATTCACATCCACCACTTCGGCTTCCGATCCCTTC	180
Db	257	AAGGTCAGTGGCGGTGATCTGGACGAGATTTCACCTCTACCATCACCAGCTCCACAC	316
Oy	181	TCGCTTCAGTGGCGGTGGGTCTGGACCTCTTACTCTCTCAGTCAGTCAGAGAGTGGAGC	240
Db	317	TGAAGATTTCGACTTACTTACTTTTCAGCAGAGTTTACAGTCTCATTCAGAAAGTTGGCC	376
Oy	241	TGAAGATCTGCTGACCTTATTACTGCGACAGTGAGTGATGACCCACCCACG-TCGCGAG	299
Db	377	AAGGACCAAGTGGAAATCAA	398
Oy	300	GGGGTCCACAGCTGGAAATCAA	321
RESULT	10		
LOCUS	AA295941	253 bp	EST
DEFINITION	EST101165 Thymus III Homo sapiens cDNA 5' end similar to similar to		
	immunoglobulin kappa light chain, V region (GB:Y00640), mRNA		
ACCESSION	AA295941		
NID	91948286		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;		
	Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae;		
	Homo.		
REFERENCE	1 (bases 1 to 253)		
AUTHORS	Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,		
	Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,		
	White,O., Sutton,G., Blake,J.A., Brannon,R.C., Man-Whi,C.,		
	Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,		
	Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Georgagen,N.S.,		
	Glodde,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,		
	Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaro,S.M., Merrick,J.M.,		
	Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,		
	Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shirley,R.,		
	Small,K.V., Spriggs,T.A., Uterback,T.R., Weidman,J.F., Li,Y.,		
	Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,		
	Dinke,D., Feng,D.-F., Ferlie,A., Fischer,C., Hastings,G.A.,		
	He,M.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,		
	Kozak,D.L., Kunsch,C., Hungjun,T., Li,H., Meisner,P.S., Olsen,H.,		
	Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.-L., Ruden,S.M.,		
	Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,		
	Fraser,C.M. and Venter,J.C.		
TITLE	Initial assessment of human gene diversity and expression patterns		
JOURNAL	based upon 83 million nucleotides of cDNA sequence		
MEDLINE	Nature 377 (6547 suppl), 3-174 (1995)		
COMMENT	96026280		
	Contact: Kerlavage, AR		
	Bioinformatics		
	The Institute for Genomic Research		
	9712 Medical Center Drive, Rockville, MD 20850 USA		
	Tel: 3018699056		
	Fax: 3018699423		
	Email: arkerlav@tigr.org		
	For clone availability, additional sequence and expression		
	information related to this EST, please check the TIGR Human Gene		
	Index (http://www.tigr.org/tdb/ngi/ngi.html)		
	Seq primer: M13 Reverse.		
FEATURES	Location/Qualifiers		
SOURCE	1. 253		
	/organism="Homo sapiens"		
	/note="Organ: thymus; Vector: pbluescript SK-; Site_1:		
	ECORI: Site_2: XhoI"		
	/db_xref="ATCC (lnost):191388"		
	/db_xref="taxon:9606"		
	/clone_lib="Thymus III"		

BASE COUNT	63 a	69 c	65 g	53 t	3 others
ORIGIN					
Query Match	24.3%; Score 78; DB 24; Length 253;				
Best Local Similarity	66.7%; Pred. No. 4,66e-105;				
Matches 146; Conservative 1; Mismatches 72; Indels 0; Gaps 0;					
Db	13	CTGTATACACAGAAACTGTGGCCAGAGTCCCAAGGCTCTCTATATCTATGTGATCCACACAG	72		
Qy	103	CTGTATACACAGAGAGAGAGATCCCTCCCAAACTTGATTTTATACATCAATCCACT	162		
Db	73	GCCCATGTGATCCACAGCAGTTCAGTGGCAGTGGGTGGGACAGAGTTCAC	132		
Qy	163	KGCTTCTGAGTCCCTGCTGCTTCTAGTGGCGGTGGGTGGGACCTTCTCTCTAC	222		
Db	133	CATAGACGCTCGACGTCTGAGATATTTTTCAGTTTATATCTGACGATATAAACTG	192		
Qy	223	AGTGAAGAGATGAGAGCTGAAATCTCCACTTATATCTGACGAGTGAAGTCTG	282		
Db	193	GCCAGAGACCTTGGCCAGGACAGCAGAGTGAATCA	231		
Qy	283	CCCAACCACTTGGAGAGGGGTCCAACTGGAATATA	321		
RESULT	11				
LOCUS	AA295093	370 bp	mrna	EST	18-APR-1997
DEFINITION	EST100400 Panceas tumor 1 Homo sapiens cDNA 5' end similar to similar to immunoglobulin kappa, variable region (GB:Y00640), mRNA sequence.				
ACCESSION	AA295093				
NID	G1947582				
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
REFERENCE	1 (bases 1 to 370)				
AUTHORS	Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Feldner,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weissbrock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brando,R.C., Man-Val,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fitcham,J.L., Georghiades,N.S., Glodok,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palancas,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudak,D.M., Shirley,R., Small,K.V., Spilligs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Fertle,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H., Raymond,L.J., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.				
TITLE	Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence				
JOURNAL	Nature 377 (6547 Suppl), 3-174 (1995)				
MEDLINE	96026280				
COMMENT	Other-ESTs: THC168243 Contact: Kerlavage, AR Bioinformatics The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850 USA Tel: 3018699056 Fax: 3018699423 Email: arkerlav@tigr.org For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/cdb/hgi/hgi.html) Seq primer: M13 Reverse.				

FEATURES		Location/Qualifiers
SOURCE		1..370 /organism="Homo sapiens" /note="Organ: pancreas; Vector: pBluescript SK-; Site_1: ECORI; Site_2: XhoI" /db_xref="ATCC (inhost):199705" /db_xref="taxon:9608" /clone_id="pancreas tumor I" /dev_stage="adult" <1..>370
BASE COUNT	85 a 107 c 94 g 77 t 7 others	
ORIGIN		
Query Match	24.3%; Score 78; DB 24; Length 370;	
Best Local Similarity	67.3%; Pred. No. 4,66e-105;	
Matches	175; Conservative 1; Mismatches 80; Indels 4; Gaps 3;	
Db	57 TGAGGCAANTMCCAGCACCCTGTGCCGTTCACAGGGGA-AAGAGCACCTCTCTTGC 115	
QY	14 TGACCCACTCTCCAGCATCTCTGTGCATCTCCAGGGAGAAGGTACACAATGACTTGC 73	
Db	116 AGGGCGACTGACAGGTATGAGAGAACCTTAGCTGGTACAGCAGAACTCGGCCAGCA 175	
QY	74 AAGGCCACCCCAAGTGT-A--AGTTACATGACTGCTGTATCAGCAGAACCCAGATCTTCC 130	
Db	176 CCCAGGCTCTNATCTATNATGATCATCCACGAGGCCACTGTATCCAGCCAGGTTTCACT 235	
QY	131 CCCAACCCTTGATTTATTACACATCCAACTCCGCTTGGAGTCCGCTCGCTTCACT 190	
Db	236 GGCACTGGGCTTGGGACAGAGTTCACTCTCACCATCAGCAGGCTTCACTGATGATCT 295	
QY	191 GCGCGTGGCTGTGGGACCTCTTACTCTCTCACAGTACAGCAGAGTGGAGGCTGAATGATCT 250	
Db	296 GCAGTTTATTACTGACGCA 315	
QY	251 GCCACTTATTACTGCGACGA 270	
RESULT 12		
LOCUS	AA295311 328 bp mRNA EST 18-APR-1997	
DEFINITION	EST100471 Pancreas tumor 1 Homo sapiens cDNA 5' end similar to immunoglobulin kappa light chain, VJ regions, mRNA sequence.	
ACCESSION	AA295311	
NID	q1947646	
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
	Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 328)	
REFERENCE	Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bul,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brannon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Frichman,J.L., Geoghegan,N.S., Glodet,K.A., Gnehm,C.L., Hanna,M.C., Hadow,E., Hinkle,P.S.Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Matmaros,S.M., Merrick,J.M., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudak,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Uterback,T.R., Weldon,J.F., Li,Y., Beharri,L.D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dinkel,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kodak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H., Raymond,D., Wei,Y.F., Wing,J., Xu,C., Yu,G.-L., Ruben,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.	
TITLE	Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cdna sequence	
JOURNAL MEDLINE	Nature 377 (6547 Suppl), 3-174 (1995)	
COMMENT	Other_Ests: THCl69106	

|||||
QY 544 CCAGAGTTCAAGGGCAAGGCCACATTACTATACACAGTCTCCAGACAGCTTACAT 603
Db 603 GGAGCTCTCACTGTACATCTGAGACTCTGCACTCTATTACTGTCAAGAGGGTTAC 662
QY 604 GGAGCTCTCACTGTACATCTGAGACTCTGCACTCTATTACTGTCAAGAGGGTTAC 663
Db 663 GGAGCTCTCACTGTACATCTGAGACTCTGCACTCTATTACTGTCAAGAGGGTTAC 710
QY 664 GGAGCTCTCACTGTACATCTGAGACTCTGCACTCTATTACTGTCAAGAGGGTTAC 711

RESULT 2
LOCUS 539590 711 bp SYN 10-FEB-1993
DEFINITION anti-erbB2 immunotoxin antigen binding region [mice, Other
ACCESSION 539590
NID 9251113
KEYWORDS
SOURCE Mus sp.
ORGANISM Mus sp.
REFERENCE 1 (bases 1 to 711)
AUTHORS Batra,J.K., Kasprzyk,P.G., Bird,R.E., Pastan,I. and King,C.R.
TITLE Recombinant anti-erbB2 immunotoxins containing pseudomonas exotoxin
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89 (13), 5867-5871 (1992)
MEDLINE 9235198
REMARK Genbank staff at the National Library of Medicine created this entry [NCBI g1bpg 108547] from the original journal article.
This sequence comes from Fig. 1.
Location/Qualifiers
1..711
/organism="Mus sp."
/db_xref="taxon:10095"
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/partial
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/note="This sequence comes from Fig. 1."
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HGKLEWIGLINPNDNYNOKRKATFTVDKSSSTAYMELLSLSDSAVYYCAR
RYDMWYFDVMGAGTTVTS"
BASE COUNT 175 a 182 c 190 g 164 t
ORIGIN

Query Match 100.0% Score 348; DB 31; Length 711;
Best Local Similarity 100.0% Pred. No. 6,18e-258;
Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 603 GGAGCTCTCACTGTACATCTGAGACTCTGCACTCTATTACTGTCAAGAGGGTTAC 662
QY 604 GGAGCTCTCACTGTACATCTGAGACTCTGCACTCTATTACTGTCAAGAGGGTTAC 663
Db 663 GGAGCTCTCACTGTACATCTGAGACTCTGCACTCTATTACTGTCAAGAGGGTTAC 710
QY 664 GGAGCTCTCACTGTACATCTGAGACTCTGCACTCTATTACTGTCAAGAGGGTTAC 711

RESULT 3
LOCUS MMU37860 336 bp mRNA ROD 16-MAR-1996
DEFINITION mRNA, partial cds.
ACCESSION U37860
NID g1127634
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus.
REFERENCE 1 (bases 1 to 336)
AUTHORS Caton,A.J., Swartzentruber,J.R., Kuhl,A.L., Carding,S.R. and
Stark,S.E.
TITLE Activation and negative selection of functionally distinct subsets
of antibody-secreting cells by influenza hemagglutinin as a viral
and a neo-self antigen
JOURNAL J. Exp. Med. 183 (1), 13-26 (1996)
MEDLINE 96136744
REFERENCE 2 (bases 1 to 336)
AUTHORS Swartzentruber,J.R.
TITLE Direct Submission
JOURNAL Submitted (10-OCT-1995) Jennifer R. Swartzentruber, The Wistar
Institute, 3601 Spruce St., Philadelphia, PA 19104, USA
Location/Qualifiers
1..336
/organism="Mus musculus"
/isolate="h922-163"
/strain="BALE/c"
/db_xref="taxon:10090"
/cell_type="B-lymphocyte"
1..336
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/product="rearranged immunoglobulin heavy chain variable
region"
/db_xref="PID:g1127635"
/translation="ELVKGASMKISCKASGVFTGYTNMWWYKSHKLEWIGLINP
YNGCTSYNOKFKKATLTYDKSSSTAYMELLSLSDSAVYYCARMLRYFDVMGAG
TTVTSYSAKT"
BASE COUNT 92 a 81 c 85 g 78 t
ORIGIN

Query Match 81.0% Score 282; DB 28; Length 336;
Best Local Similarity 95.1% Pred. No. 7.81e-203;
Matches 308; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

OY	629	GACTGTGAGCTTATTACTGTGCAG -GAGGGTTACGAGCTGTACTTCGATGTCTGGGG	687
DB	300	CGCAGGACCAACGCTCACCGTCTC	323
OY	688	CGCAGGACCAACGCTCACCGTCTC	711
RESULT	4	578745	354 bp mRNA ROD 28-OCT-1995
LOCUS			
DEFINITION		Ig VH-anti-phosphatidylserine monoclonal antibody PS4A7 heavy chain variable region [mice, hydridoma, mRNA Partial, 354 nt].	
ACCESSION		578745	
NID		91041920	
KEYWORDS			
SOURCE		Mus sp., hydridoma.	
ORGANISM		Mus sp.	
REFERENCE		Mus.	
AUTHORS		1 (bases 1 to 354)	
TITLE		Igarashi,K., Asai,K., Kaneda,M., Umeda,M. and Inoue,K. Specific binding of a synthetic peptide derived from an antibody complementarily determining region to phosphatidylserine	
JOURNAL		J. Biochem. 117 (2), 452-457 (1995)	
MEDLINE		95332275	
REMARK		Genbank staff at the National Library of Medicine created this entry [NCBI gisbq 169252] from the original journal article.	
FEATURES		Location/Qualifiers	
source		1..354	/organism="Mus sp."
gene		1..354	/db_xref="taxon:10095"
CDS		1..354	/partial /note="anti-phosphatidylserine monoclonal antibody PS4A7 heavy chain variable region" /gene="Ig VH"
		1..354	/partial /gene="Ig VH" /note="This sequence comes from Fig. 1A. Protein sequence is in conflict with the conceptual translation; mismatch(35[K->N])"
		1..354	/codon.start=1 /product="anti-phosphatidylserine monoclonal antibody PS4A7 heavy chain variable region" /translation="EVDLOQSGPELVKPGASMKISCKASGYFTGMTKKWVSHGRNKLEWIGLIPNGSTSYNOKEFKRATLITVDKSSPAYVELLSLTSDSAVYYCCAREGDYDGANDYWGOCSTSVYS"
BASE COUNT		96 a 84 c 92 g 82 t	
ORIGIN			
Query Match		76.1%; Score 265; DB 28; Length 354;	
Best Local Similarity		90.0%; Pred. No. 1,05e-188;	
Matches	315; Conservative	0; Mismatches 32; Indels 3; Gaps 2;	
DB	4	GTTCAGCTGCACACAGCTGTGAGCTTAGCTGGTGGAAGCTCGAGCTTCACATGAAGTATCC	63
OY	365	GTGCAGCTTCAGAGAGCTCAGACCTTAGAGGCTGGAAGCTTCGATGAAGATATCC	424
DB	64	TGCAGAGCTTCGTGGTTACCATTCACCTAGCTGCTACACCATTAAGTGGGTGAAGCAGGCCAT	123
OY	425	TGCAGAGCTTCGTGGTTACCATTCACCTAGCTGCTGCGCCACACCATTAAGTGGGTGAAGCAGGCCAT	484
DB	124	GGAAAGAACCCTTGAGTGCATTGACTATTAATCCTTACATATGTTGGTACTAGCTACAAC	183
OY	485	GGAAAGAACCCTTGAGTGCATTGACTATTAATCCTTACATATGTTGGTACTAGCTACAAC	544
DB	184	CAGAAGTTCAAGGGCAGGCCACATTAACTAGAACAAAGTCTTCACAGCAGACCTTACATG	243
OY	545	CAGAAGTTCAAGGGCAGGCCACATTAACTAGAACAAAGTCTTCACAGCAGACCTTACATG	604

	Db	244	GAGCTCCTCAgTCTGACATCTGCATGACTCTGTCCAGTCATTATTA	303
	Oy	605	GAGCTCCTCAgTCTGACATCTGCATGACTCTGTCCAGTCATTATTA	661
	Db	304	TACGACGGGGCGCTATGAGTACTTGCGGTCAAGAACCTTAGTACC	353
	Oy	662	ACGGAAGTCTGATCTGATGTCTGGGGCGGACGACGATCACCGTCTC	711
	RESULT	5		
	LOCUS	MNU25678	351 bp	mRNA
	DEFINITION	Mus musculus Ig heavy chain variable region		partial cds.
	ACCESSION	U25678		
	NID	9847823		
	KEYWORDS	.		
	SOURCE	house mouse.		
	ORGANISM	Mus musculus		
		Eukaryota; Eukarya; Eumetazoa; Vertebrata; Mammalia; Muridae; Mus.		
	REFERENCE	1 (bases 1 to 351)		
	AUTHORS	Liu, J., Wu, W., Wang, B., Pan, Z., Tian, P., Huang, Z. and Hong, J.		
	TITLE	Cloning and sequencing of immunoglobulin heavy variable-region gene by polymerase chain reaction		
	JOURNAL	Sheng Wu Hua Hsueh Tsa Chih 9 (No.1), 70-75 (1993)		
	AUTHORS	Xu, L.		
	TITLE	Direct Submission		
	JOURNAL	Submitted (21-APR-1995) Lin Xu, Institute of Biophysics, Academia Sinica, Dept. of Protein Engineering, 15 Datun Road, Chaoyang District, Beijing 100101, Peoples Republic of China		
	FEATURES	location/Organism		
	source	1..351		
		/organism="Mus musculus"		
		/db_xref="taxon:10090"		
	CDS	<1..>351		
		/codon_start=1		
		/label="c1077		
		/product="immunoglobulin heavy chain variable region"		
		/db_xref="PID:g847824"		
		/translation="QVQLQQSGPELVYPGASMKISCTSGSYFGLTMNYKOSHEN LEWIGLINPYSGGTINYOKFRKRTVLVDSSSTAYMELLSTSEDAVYYCARYSK AMDYWGOTTVTASS"		
	BASE COUNT	98 a 88 c 84 g 81 t		
	ORIGIN			
	Query Match	75.9%; Score 264; DB 28; Length 351;		
	Best Local Similarity	90.2%; Pred. No. 7, 10e-18;		
	Matches	313; Conservative 0; Mismatches 31; Indels 3; Gaps 2;		
	Db	4	GTCCAAGTCTGACATCTGCATGACTCTGTCCAGTCATTATTA	63
	Oy	365	GTGCAAGTCTGACATCTGCATGACTCTGTCCAGTCATTATTA	424
	Db	64	TCCAAGTCTTGTGTTACTCATTTACTGCTGCTAACCATACTGGGTAAAGCAGCCAT	123
	Oy	425	TCCAAGTCTTGTGTTACTCATTTACTGCTGCTAACCATACTGGGTAAAGCAGCCAT	484
	Db	124	GAAGAAGACCTTGAAGTGGATGACTTATTAATCTTACAGTGGTGTACTACTACAAC	183
	Oy	485	GAAGAAGACCTTGAAGTGGATGACTTATTAATCTTACAGTGGTGTACTACTACAAC	544
	Db	184	CAGAAGTCTCAAGGAGGCCACATTAACTGTAGACAGTAGTCATCCAGACAGCCATACG	243
	Oy	545	CAGAAGTCTCAAGGAGGCCACATTAACTGTAGACAGTAGTCATCCAGACAGCCATACG	604
	Db	244	GAGCTCCTCAgTCTGACATCTGCATGACTCTGTCCAGTCATTATTA	302
	Oy	605	GAGCTCCTCAgTCTGACATCTGCATGACTCTGTCCAGTCATTATTA	664
	Db	303	TAAAGCTA--TGACTACTGGGGCCAAAGGACACAGGTACACCGTTC	347
	Oy	665	GACTGTACTCTGATGTCTGGGGCCAAAGGACACAGGTACACCGTTC	711

RESULT	6	MMAHCVR2	354 bp	DNA	ROD	07-OCT-1996
LOCUS						
DEFINITION		M.musculus antibody heavy chain variable region (354bp).				
ACCESSION		X90877				
NID		g1518294				
KEYWORDS		antibody heavy chain; variable region.				
SOURCE		house mouse.				
ORGANISM		Mus musculus				
		Eukaryota; mitochondria eukaryotes; Metazoa; Chordata;				
		Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;				
REFERENCE		Mus.				
AUTHORS		1 (bases 1 to 354)				
JOURNAL		Geiser/M. and Kretzschmar/T.				
REFERENCE		Unpublished				
AUTHORS		2 (bases 1 to 354)				
TITLE		Geiser/M.				
JOURNAL		Direct Submission				
		Submitted (17-AUG-1995) M. Geiser, CIBA-GEIGY LTD, CDDT,				
		K-681.5.45, CH-4002, Basel, SWITZERLAND				
FEATURES		Location/Qualifiers				
SOURCE		1..354				
		/organism="Mus musculus"				
		/strain="Balb/c"				
		/db_xref="taxon:10090"				
		/dev_stage="12 weeks old"				
		/tissue_type="spleen"				
		/cell_type="lymphocytes"				
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CDS		/codon_start=1				
		/product="antibody heavy chain variable region"				
		/db_xref="PID:e264666"				
		/db_xref="PID:g1518295"				
		/translation="EVKLOQSPPELVKPGASVKMSCKASGYFTDYMKRWKSHGKS				
		LWIMGIDIPNNNGDFEYNQKFKGKATLIVDKSSSTAYMQLNSLSSESAVYYCANDGYH				
		MYFDWGSGTPVTYS"				
BASE COUNT		92 a 89 c 93 g 80 t				
ORIGIN						
Query Match		75.3%; Score 262; DB 28; Length 354;				
Best Local Similarity		89.1%; Pred. No. 3,24e-186;				
Matches		310; Conservative 0; Mismatches 36; Indels 2; Gaps 2;				
Db	4	GTCAGCTGCACACGTGGGACCTGACTGGTGGAAGCCCGGCTCATGTAAGATGCC	63			
Oy	365	GTCAGCTGCACACGTGCAGACCTGAGGCTGAGAACCTCGAAGTTCAATGAAGATATCC	424			
Db	64	TGCAGGCTTCGTGATACACTCTTACTGACTACATGATGAGTGGTAGAGAGACCATT	123			
Oy	425	TGCAGACTTTGTGTACTTACTTACTGCTGACACACCATGAACTGGGTGAAGCAGACCAT	484			
Db	124	GGAAGAGCCTTGATGATTTGAGATATTATTCCTAACAAATGGTATCTTCTTACAAC	183			
Oy	485	GGAAGAACCTTGAATGGATGACTATTAATCCTTACAATGGTATCTTACTAATAACAAC	544			
Db	184	CAGAGTTCAAGGAGGACCATTTGATGATGAGACAAATCTCCGACGACAGCTACATG	243			
Oy	545	CAGAGTTCAAGGAGGACGACCATTTTACTGTAGACAAATCGTCCAGCACAGCTTACATG	604			
Db	244	CAGCTCAACAGCCTGACATCTGAGGAGCTGAGCTATTTACTGTGCCAATGATGGTTAC	303			
Oy	605	GAGCTCTCAGTCTGACATCTGAGGAGCTGAGCTATTTACTGTATCTAGTGC - AAGGAGGGTTAC	663			
Db	304	C-ACGTGTAATCTGATGCTGTGGGGGCGCAGGACACCCCCTGACCGTCTC	350			
Oy	664	GGAGTGTACTTCGATGCTGTGGGGGCGCAGGACACCGGTACCGTCTC	711			
RESULT	7	S7A055	355 bp	mRNA	ROD	01-MAR-1995
LOCUS						
DEFINITION		Igc VH IIA-igkb2 VH region [mice, transfected Sp2/0 myeloma cells,				
		mRNA Recombinant Partial, 355 nt].				

ACCESSION	S74055
NID	6688162
KEYWORDS	
SOURCE	
ORGANISM	Mus sp. transfected Sp2/0 myeloma cells.
REFERENCE	Mus sp. Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sclirognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 355)
TITLE	Mount, P.F., Sutton, V.R., Li, W., Burgess, J., McKenzie, I.F., Pietersz, G.A. and Trapani, J.A. Chimeric (mouse/human) anti-colon cancer antibody c30.6 inhibits the growth of human colorectal cancer xenografts in scid/scid mice
JOURNAL MEDLINE	Cancer Res. 54 (23), 6160-6166 (1994)
REMARK	95042371
FEATURES	GenBank staff at the National Library of Medicine created this entry [NCBI gidsbq 157470] from the original journal article. This sequence comes from Fig. 1A.
SOURCE	Location/Qualifiers
gene	1..355
	/organism="Mus sp."
	/db_xref="taxon:10095"
	1..354
	/partial
	/note="IgG2b VH region"
	/gene="IgG V<down>H</down> IIA"
	1..354
	/partial
	/gene="IgG VH IIA"
	/note="chimeric anti-colon cancer monoclonal antibody c30.6/IgG heavy chain variable region; chimeric mouse/human. This sequence comes from Fig. 1A"
	/codon_start=1
	/product="IgG2b VH region"
	/db_xref="PID:g688163"
	/translation="QVLOESGPELVKPGASVKRISKASGVTETDYMHWKSHGSKS LEMIGFLPYRNAGIGYKQKRNKATLLIVDSSSLAIYMLSLISEDSAVYICTRNDPH WYFVWQGGITLVSS"
BASE COUNT	93 a 92 c 90 g 80 t
ORIGIN	
Query Match	74.4%; Score 259; DB 28; Length 355;
Best Local Similarity	87.3%; Pred. No. 1.00e-183;
Matches 303; Conservative	0; Mismatches 44; Indels 0; Gaps 0;
4	GTCCACTGTCAGAGAGTCAGGCTGAGCTGGTGAACCTGGGGCTCAGTAAGATATCC 63
365	GTGCGAGTCGACGAGATCAGACCTGAGTGGTGAAGCTCGAGGTTCAATGAAGATATCC 424
64	TGCAGGCTTCGTGATACATCTTCACTGACGTCAACATGACACTGGGTGAAGCAGACCAT 123
425	TGCAGAGCTTCGTGATTACTATCTACTGGCCACACCATGAGTAAGTGGTGAAGCAGACCAT 484
124	GGAAGAGCTTCGTGATGATGATGATTTTATTCCTTACATTCGCTGACTGCTACAC 183
485	GGAAGAGCTTCGTGATGATGATGATTTTATTCCTTACATTCGCTGACTGCTACAC 544
184	CAGAAATTCAGAAACGACCATTCGATGAGTGAAGACCTTCCTCCAGACAGCCATATG 243
545	CAGAAATTCAGAAACGACCATTCGATGAGTGAAGACCTTCCTCCAGACAGCCATATG 604
244	GAGCTCCGACAGCTGACATCTGAGGAGCTCCAGTCTATTACTGTACAAAGAAATGACCCC 303
605	GAGCTCCGACAGCTGACATCTGAGGAGCTCCAGTCTATTACTGTACAAAGAAATGACCCC 350
304	CACTGTACTTCTGTTGTTGGGGCCAGGACCAAGCAGGTCACCGCTCTC 350
665	GACTGTACTTCTGATGTCTGGGGGCGCAGGAGCAACGAGTCAACCGTCTC 711
RESULT	8
LOCUS	MUSCWMG 357 bp mRNA
DEFINITION	Mouse mRNA sequence, partial cds.
	ROD 30-JUN-1993

ACCESSION	N65944
NID	g309176
KEYWORDS	Mus musculus (strain BALB/c, sub_species domesticus) cDNA to mRNA
SOURCE ORGANISM	Mus musculus Mus musculus Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE AUTHORS	1 (bases 1 to 357) Simpson,J.A., Chow,J.C., Baker,J., Avdalovic,N.M., Yuan,S., Co,M.S., Vasquez,M., Britl,W.J. and Coellingh,K.L.
TITLE	Untitled
JOURNAL	Unpublished (1992)
FEATURES	Location/Qualifiers source 1..357 /organism="Mus musculus" /strain="BALB/c" /sub_species="domesticus" /db_xref="taxon:10090" /cell_line="MAB 5" /cell_type="hybridoma" mat_peptide 1..357 /note="putative"
BASE COUNT	96 a 87 c 88 g 86 t
ORIGIN	
Query Match	74.4%; Score 259; DB 28; Length 357;
Best Local Similarity	89.1%; Pred. No. 1,00e-183;
Matches 312; Conservative 0; Mismatches 35; Indels 3; Gaps 2;	
Db 4	GTCAGCTGCAACAGTGTGGACTGACCTGAGCTGGTGAAAGCTTGAGCTTCAATGAAGATATCC 63
Oy 365	GTCGAGCTGCAGAGTCAGACCTGAGAGTGGTGAAGCCTCGAGGTTCAATGAAGATATCC 424
Db 64	TGCAAGCTTGTGTTTACTATTACTAGCTACACCATGAACCTGGGTGAAGCACGACCAT 123
Oy 425	TGCAGAGCTTGTGGTTACTATTACAGGCCAACCATGGAACGGGTGAAGCACGACCAT 484
Db 124	GGACAGAACCCTTGATGGATGGAGCTAATTAATCCTACAAGTGGGTACTACTACCAAC 183
Oy 485	GGANAGAACCTTGATGGATGGAGCTAATTAATCCTACAAGTGGGTACTACTACCAAC 544
Db 184	CAGAAGTTCAGGGGGAAGGCCACATTACTAGTAGACAGTATCAACAGCAGCCTACATG 243
Oy 545	CAGAAGTTCAGGGGGAAGGCCACATTACTAGTAGACAGTATCAACAGCAGCCTACATG 604
Db 244	GAGCTCTCTAGCTGTGACATCTGGCGAGCTGTGCAGCTATTACTGTACAGACGGGGTTT 303
Oy 605	GAGCTCTCTAGCTGTGACATCTGAGAGCTTGCAGTCTATTACTGTGTCAG--GAGGGTTA 662
Db 304	CGAGACTTCTATGAGACTACTGGGGTCAGAGAACTCAACCTCAACCGCTTC 353
Oy 663	CG-GACTGTACTCTTGATGTTGGGGGCGAGGACCAACGCTCAACCGCTTC 711
RESULT 9	178572 414 bp DNA PAT 23-DEC-1997
LOCUS	178572
DEFINITION	Sequence 84 from patent US 5693761.
ACCESSION	178572
NID	g3014726
KEYWORDS	
SOURCE	Unknown.
ORGANISM	Unknown. Unclassified.
REFERENCE	1 (bases 1 to 414) Queen,C.L., Schneider,W.P. and Selick,H.E.
AUTHORS	Polynucleotides encoding improved humanized immunoglobulins
TITLE	Patent: US 5693761-A 84 02-DDC-1997;
JOURNL	Location/Qualifiers
FEATURES	1..414 /organism="unknown"
BASE COUNT	105 a 102 c 103 g 104 t
ORIGIN	

Query Match	74.4%;	Score 259;	DB 21;	Length 414;
Best Local Similarity	89.1%;	Pred. 1.00e-183;		
Matches 312;	Conservative	0;	Mismatches 35;	Indels 3;
			Gaps 2;	
Db 61	GMCCAGCTGCACAACACTCTGGACCTGAGCTGGGGAAGCCTGGAGGCTTCATGAAAGTATCC	120		
Qy 365	GTGCGAGCTGCAGAGACTCAGGACCTTAGAGTGGTGAAGCTTGAGGTTCAATAGATATCC	424		
Db 121	TGCAGGCTCTGTCTTACTCATATTCAGTGGCTACACCATGAACCTGGGTGAAGCAGACCAT	180		
Qy 425	TGCAGAGCTCTGTGTTACTCATATTCAGTGGCCACACCATGAAGCTGGGTGAAGAGCCAT	484		
Db 181	GGACAGAACCTTGAATGGATTGGACTATTATATCTTCAATGGTGGTACTAGCTACAC	240		
Qy 485	GGAAAGAACCTTGAATGGATTGGACTATTATATCTTCAATGGTGGTACTAGCTACAC	544		
Db 241	CAGAGTTCAGAGGGGAAGGCCACATTACTGTAGACAGATCATCCACACAGCCCTACATG	300		
Qy 545	CAGAGTTCAGAGGGGAAGGCCACATTACTGTAGACAGATCATCCACACAGCCCTACATG	604		
Db 301	GAGCTCTCAGTCTGACATCTGCGGACTCTCAGTCTATTACTGTACAAAGACGGGGGTTT	360		
Qy 605	GAGCTCTCAGTCTGACATCTGAGGACTCTGAGTCTATTACTGTACAAAG--GAGGGTTA	662		
Db 361	CGAGCTATTTCTATGAGCTACTGGGGGTAAAGAACCTTAGTCACCGCTTC	410		
Qy 663	CG-GAGTCTACTTGTGATGTCTGGGGGCCAGAGCCAGGCTACCGTCTC	711		
RESULT 10	I78627	414 bp	DNA	PAT 23-DEC-1997
LOCUS	Sequence 84	from patent US 5693762.		
DEFINITION	I78627			
ACCESSION	g3014781			
NID				
KEYWORDS	Unknown.			
SOURCE	Unknown.			
ORGANISM	Unclassified.			
REFERENCE	1 (bases 1 to 414)			
AUTHORS	Queen, C.L., Co, M. Sung, Schneider, W.P., Landolfi, N.F., Coelinhg, K.L.			
TITLE	Humanized immunoglobulins			
JOURNAL	Patent: US 5693762-A 84-02-DEC-1997;			
FEATURES	Location/Qualifiers			
source	1..414			
BASE COUNT	105 a 102 c 103 g 104 t			
ORIGIN				
Query Match	74.4%;	Score 259;	DB 21;	Length 414;
Best Local Similarity	89.1%;	Pred. No. 1.00e-183;		
Matches 312;	Conservative	0;	Mismatches 35;	Indels 3;
			Gaps 2;	
Db 61	GMCCAGCTGCACAACACTCTGGACCTGAGCTGGGGAAGCCTGGAGGCTTCATGAAAGTATCC	120		
Qy 365	GTGCGAGCTGCAGAGACTCAGGACCTTAGAGTGGTGAAGCTTGAGGTTCAATAGATATCC	424		
Db 121	TGCAGGCTCTGTCTTACTCATATTCAGTGGCTACACCATGAACCTGGGTGAAGCAGACCAT	180		
Qy 425	TGCAGAGCTCTGTGTTACTCATATTCAGTGGCCACACCATGAAGCTGGGTGAAGAGCCAT	484		
Db 181	GGACAGAACCTTGAATGGATTGGACTATTATATCTTCAATGGTGGTACTAGCTACAC	240		
Qy 485	GGAAAGAACCTTGAATGGATTGGACTATTATATCTTCAATGGTGGTACTAGCTACAC	544		
Db 241	CAGAGTTCAGAGGGGAAGGCCACATTACTGTAGACAGATCATCCACACAGCCCTACATG	300		
Qy 545	CAGAGTTCAGAGGGGAAGGCCACATTACTGTAGACAGATCATCCACACAGCCCTACATG	604		
Db 301	GAGCTCTCAGTCTGACATCTGCGGACTCTCAGTCTATTACTGTACAAAGACGGGGGTTT	360		
Qy 605	GAGCTCTCAGTCTGACATCTGAGGACTCTGAGTCTATTACTGTACAAAG--GAGGGTTA	662		
Db 361	CGAGCTATTTCTATGAGCTACTGGGGGTAAAGAACCTTAGTCACCGCTTC	410		
Qy 663	CG-GAGTCTACTTGTGATGTCTGGGGGCCAGAGCCAGGCTACCGTCTC	711		

FEATURES	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523
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	SOURCE	1..366 /organism="Mus musculus" /strain="BALB/c" /db_xref="taxon:10090" /note="immunized with HIV-1 viral lysate"
CDS		<1..>366 /codon_start=1 /product="anti-HIV-1 p24 single chain antibody A2 Ig heavy chain variable region" /db_xref="PID:g3493269" /translation="OVOLQOOSGPELVKPGASVKLSCKLSGYSPFTYTMWVKKSHGKNLEWIGLIPYNPGRNNOKFEGKATFLVDKSSSTAYMELLISLSEDSAVYYCARDPRYYGSSMYDWMAGTTPYVS"
BASE COUNT	91 a	91 c 95 g 89 t
ORIGIN		
Query Match	72.4%	Score 252; DB 28; Length 366;
Best Local Similarity	93.8%;	Pred. No. 6 36e-178;
Matches	270; Conservative	0; Mismatches 18; Indels 0; Gaps 0;
Db	4	GTTCACTGCACGACTGTGGCCCTGAGCTGTGTGAAGCCTGGGGCTTCAGTAGTGTC
Oy	365	GTGCGAGTCGAGGAGTACGAGACCTGAGGCGTGAAGCCTGGAGGTTCAATGAATATCC
Db	64	TGCAAGCTTCTGCTTACTATTCTACTGCTACCTGCGTCAACCATGAACTGGGTGAAGCACCAT
Oy	425	TGCAAGACTTCTGCTTACTATTCTACTGCTACCTGCGCACCATGAACTGGGTGAAGCACCAT
Db	124	GGAAGAAGCTTGAATGTGATTTAATCTTCAATGATGATTAAGAACAC
Oy	485	GGAAAAGACCTTGATGTGACTTTATTAATCTTCAATGATGATTAAGAACAC
Db	184	CAGAAGTCAAGGCGAAGGCCACATTAACTTAGACAAGTCATCCAGCAGACCTTACATG
Oy	545	CAGAAGTCAAGGCGAAGGCCACATTAACTTAGACAAGTCATCCAGCAGACCTTACATG
Db	244	GAGCTCCTAGTCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCA
Oy	605	GAGCTCCTAGTCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCA
RESULT	15	
LOCUS	MUSHA4	440 bp mRNA ROD 24-JUL-1991
DEFINITION	Mouse active H-chain VJ region, 5' cds.	
ACCESSION	M74137	
NID	G193744	
KEYWORDS	J-region; V-region; immunoglobulin heavy chain.	
SOURCE	Mus musculus cDNA to mRNA.	
ORGANISM	Mus musculus	
REFERENCE	Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata; Vertebrates; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.	
AUTHORS	I (bases 1 to 440)	
TITLE	Rueff-Juy,D., Marche,P.N., Drepier,A.-M. and Cazenave,P.-A.	
JOURNAL	Functional diversity of H and L chains allows the coexpression of two mutually exclusive idiotopes (Id1104 and Id158)	
MEDLINE	J. Immunol. 146, 4024-4030 (1991)	
FEATURES	91237115	
SOURCE	Location/Qualifiers	
	1..440	/organism="Mus musculus"
	/db_xref="taxon:10090"	
	/cell_line="hybridoma"	
	39..440	/partial
	/codon_start=1	
	/product="Ab 16.3 heavy chain variable and joining regions"	
CDS	/db_xref="PID:g193745"	
	/translation="MEDSLSPVLRNCRLSEVOLQSGPELVKPGASVKNSCKRASCSTFTDIYIMKWVQSPKSLIEWIGDISPNNGISTYNOKFGKATFLVDKSSSTAYMOLLNLTSDSAVYYCARDPRYYGSSMYDWMAGTTPYVS"	
BASE COUNT	114 a	112 c 110 g 104 t

ORIGIN

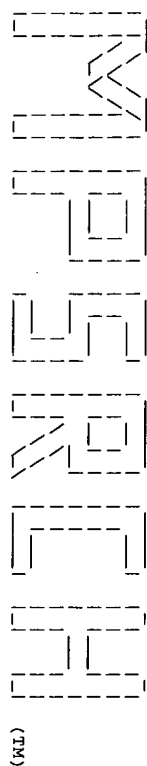
Query Match 71.88; Score 250; DB 28; Length 440;

Best Local Similarity 88.28; Pred. No. 2.88e-176;

Matches 306; Conservative 0; Mismatches 38; Indels 3; Gaps 3;

Db 93 GTCCAGCTGACACATCTGACCTGAGCTGGTAAAGCCCGGGGCTTCAGTGAAGATGTCC 152
 ||||||| || ||||||| ||| ||||||| ||| ||||||| ||| ||||||| |||
 QY 365 GTGCAGCTGCAGGAGTCAGGACCTGAGGTGGTGAAGCCTGGAGTTCAATGAGATATCC 424
 ||||||| || ||||||| || ||||||| || ||||||| || ||||||| || |||||||
 Db 153 TGTAAAGCTTGTGATACACATTCACCTACTACATGAAGTGGTGAAGCAGAGCCCT 212
 || ||| ||||||| || ||||||| || ||||||| || ||||||| || ||||||| ||
 QY 425 TGCAAGACTTCTGTACTCATTCATTCAGTGGCCACACCATGAAGTGGTGAAGCAGAGCCAT 484
 || ||| ||||||| || ||||||| || ||||||| || ||||||| || ||||||| ||
 Db 213 GGAAGAGCCTTGAGTGGATGGAGATATTAATCCTTAACATGGTGTACTAGCTACAAC 272
 ||||||| ||||||| ||||||| || ||| ||| ||||||| ||| ||||||| ||| |||
 QY 485 GGAAGAACCTTGAGTGGATGGAGTGTATTAATCCTTAACATGGTGTACTAGCTACAAC 544
 ||||||| ||||||| ||||||| || ||| ||| ||||||| ||| ||||||| ||| |||
 Db 273 CAGAAGTCAAGGGCAGAGCCACATTTGACTGTAGACAATCCCTCAGCAGAGCCTACATG 332
 ||||||| ||||||| ||||||| || ||| ||| ||||||| ||| ||||||| ||| |||
 QY 545 CAGAAGTCAAGGGCAGAGCCACATTTGACTGTAGACAATCCCTCAGCAGAGCCTACATG 604
 ||||||| ||||||| ||||||| || ||| ||| ||||||| ||| ||||||| ||| |||
 Db 333 CAGCTCAACAGCCTTACATCTGAGGACTCTGCAGTCTATTACTGTGCAAG-AGA-TTACG 390
 || ||| || ||| || ||||||| || ||||||| || ||||||| || ||||||| || |||
 QY 605 GAGCTCCTCAGTCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAGGAGGTTACG 664
 || ||| || ||| || ||||||| || ||||||| || ||||||| || ||||||| || |||
 Db 391 -ACTGTACTTGTGATGTCTGGGGCACAGGGACCAAGGTCACCGTCTC 436
 ||||||| ||||||| ||||||| || ||| ||| ||||||| ||| ||||||| ||| |||
 QY 665 GACTGTACTTGTGATGTCTGGGGCACAGGGACCAAGGTCACCGTCTC 711
 ||||||| ||||||| ||||||| || ||| ||| ||||||| ||| ||||||| ||| |||

Search completed: Sat Jan 9 15:24:33 1999
 Job time : 540 secs.



(TM)

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MPsrch_n n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Sat Jan 9 16:26:30 1999; MasPar time 64.16 Seconds
737.977 Million cell updates/sec

Tabular output not generated.

Title: >US-08-704-178-1
(364-711) from US08704178.seq (3 of 4)
Description: 348 TGTGCACTGCTGAGAGTAC.....GGGACACAGGTCACCGTCTC 711
Perfect Score: 364 TGTGCACTGCTGAGAGTAC.....GGGACACAGGTCACCGTCTC 711
N.A. Sequence: ACACGTGAGCTGCTGAGTAC.....CCCTGTGTCACGAGGAGAGAG

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 188442 segs, 68026449 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: n-geneseq32

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39 40:part40

Statistics: Mean 8.057; Variance 4.765; scale 1.691

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	348	100.0	711	29	T65006	Single-chain anti-erb
2	344	88.9	711	18	T17728	Anti-erbB2 scfv CDNA.
3	344	98.9	711	9	Q5180	Sequence encoding the
4	265	76.1	462	22	T34542	Monoclonal anti-idiot
5	265	76.1	462	21	T31541	3M1 heavy chain varia
6	265	76.1	462	38	T99435	Anti-idiotypic antibod
7	257	73.9	417	7	Q43843	Chimeric 128.1 VH, mo
8	257	73.9	10704	7	Q43846	Plasmid pRH4625.
9	257	73.9	10844	7	Q43848	Plasmid pRH4808.
10	257	73.9	11529	7	Q43844	Plasmid pRH4602.
11	257	73.9	12132	7	Q43847	Plasmid pRH4807.
12	249	71.6	443	11	Q45428	KM-750 heavy chain.
13	245	70.4	356	5	Q28522	Hypercalcaemia agent

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
14	242	69.5	717	37	T86309	Single chain anti-dis
15	242	69.5	1175	37	T86311	Single chain anti-dis
16	240	69.0	913	12	Q81076	Bispecific CD3-D6EVI9
17	235	67.5	354	11	Q65553	Mouse anti-HIV mus.5
18	235	67.5	354	12	Q70371	Anti HIV antibody hea
19	231	66.4	449	11	Q45426	KM-796 heavy chain.
20	231	66.4	1773	38	T88869	H chain subunit of Fa
21	230	66.1	729	12	Q73579	Fv(GP-4) immunosuppre
22	225	64.7	331	30	T43738	Anti-DNA antibody 8d8
23	225	64.7	334	30	T43737	Anti-DNA antibody 7b3
24	225	64.7	360	12	Q69933	scFv 07.6 heavy chain vari
25	225	64.7	360	19	T12612	scFv 07.6 VH gene.
26	225	64.7	405	5	Q30754	p12-h2.
27	225	64.7	474	2	Q12014	Sequence encoding mou
28	225	64.7	474	2	Q12058	Sequence encoding hea
29	224	64.4	424	24	T42717	HmC3 VH coding sequ
30	222	63.8	426	40	V20602	A77 anti-Fc alpha R a
31	221	63.5	372	16	T05018	PD5 antibody heavy ch
32	221	63.5	402	25	T31293	Guy's 13 anti-Strepto
33	221	63.5	450	1	Q04695	Heavy chain variable
34	220	63.2	420	40	V09796	DNA encoding the heav
35	219	62.9	360	40	V09798	DNA encoding the heav
36	218	62.6	413	24	T34153	Monoclonal antibody p
37	217	62.4	357	18	T04014	Anti-BGR antibody he
38	217	62.4	387	14	Q27141	ICAM-1 inhibiting pep
39	217	62.4	486	31	T59339	M1 monoclonal antibo
40	215	61.8	354	18	T04018	Anti-EGFR antibody he
41	213	61.2	357	31	T58254	Lead binding MAb 14F1
42	212	60.9	405	33	T78589	Monoclonal antibody 6
43	212	60.9	499	2	Q11291	Encodes murine monoc
44	212	60.9	762	17	T03381	Anti-IL-8 MAb 6G4.2.5
45	212	60.9	762	33	T78595	Chimeric monoclonal a

ALIGNMENTS

RESULT 1
ID T65006 standard; CDNA: 711 BP.
AC T65006;
DT 05-JUN-1997 (first entry)
DE Single-chain anti-erbB2 antibody e23(Fv) CDNA.
KW Single chain antibody; variable region; light chain; heavy chain;
KW breast cancer; ovarian cancer; non-small cell lung carcinoma;
KW Immunodiagnosis; treatment; cytotoxic agent; erbB-2; ds.
OS Mus musculus.
OS Synthetic.
FH Key Location/Qualifiers
FT mat-peptide 1..711
FT /tag= a
FT /product= e23(Fv)
PD US5587458-A.
PD 24-DEC-1996.
PF 07-OCT-1991: 772270.
PR 07-OCT-1991: US-772270.
PR 30-JUN-1992: US-906355.
PR 14-MAY-1993: US-061092.
PA (ARON-) ARONEX PHARM INC.
PI Bird RE, Kasprzyk PG, King CR.
PI WPI: 97-064831/06.
DR P-PSDB; M15185.
PT Single chain antibodies specific for erbB-2 protein, gp185 - with
PT labels or cytotoxin, useful for detection and treatment of tumour
PT cells expressing this protein
PS Example 8: Columns 25-28; 28bp; English.
CC The present cDNA sequence codes for a claimed single-chain antibody,
CC designated e23(Fv), which binds to erbB-2. Monoclonal antibody e23,
CC was generated by immunising mice with N/erbB-2 cells overexpressing
CC the gp185 protein, removing spleen cells and producing hybridomas
CC by standard techniques. Messenger RNA coding for the anti-erbB-2
CC monoclonal antibody was isolated and converted to cDNA. Regions
CC coding for the heavy- and light- chain variable regions were then
CC amplified by PCR and joined via a sequence encoding a peptide
CC linker. The resulting single-chain antibody is useful for in vitro


```
Db 543 ccagaagttcaagggcagggccacattactgtgacaaagtctccagacagctacat 602
      |||
Oy 544 CCAGAAAGTTCAAGGGCAGGGCCACATTACTGTAGACAAGTCGTCAGACAGGCTACAT 603
      |||
Db 603 ggagctccctcagctgacatctgagagctcgtcactctattacgtgccaaggaggttac 662
      |||
Oy 604 GGAGCTCTCTCAGTGTGACATCTGAGGACTCTGCGAGTCTATTACTGTCCAAAGAGGTTAC 663
      |||
Db 663 ggactgttactcagatctctgaggcgagggaccagagtcacgctctc 710
      |||
Oy 664 GGACTGTACTTTCATGTCTGGGCGCAGGAGCACGCTCACCGTCTC 711

RESULT 4
ID T34542 standard; cDNA: 462 BP.
AC T34542;
DT 11-OCT-1996 (first entry)
DE Monoclonal anti-idiotypic antibody 3H1 VH cDNA.
KM Anti-idiotypic antibody; monoclonal antibody; CEA.
KW carcinoembryonic antigen; tumour-associated antigen; cancer;
OS vaccine; immunotherapy; ss.
Mus sp.
FH Key Location/Qualifiers
FT cds 22..462
      /tag= a
PI WO9620219-A2.
PN 04-JUL-1996.
PF 28-DEC-1995; U17105.
PR 28-DEC-1994; US-365484.
PA (KENT ) UNIV KENTUCKY.
PI Chatterjee M, Chatterjee SK, Foon KA, Kohler H;
DR WPI: 96-321809/32.
DR P-PSDB: R99687.
PT Monoclonal anti-idiotypic antibody 3H1 - elicits an immune response
PT to carcinoembryonic antigen
PS Example 2: Fig 2A: 102pp; English.
CC A cDNA clone (T34542) codes for the heavy chain variable region
CC (R99687) of monoclonal anti-idiotypic antibody 3H1 (ATCC HB 12003).
CC It was obt'd. by PCR amplification (see also T34543-44) of cDNA
CC derived from 3H1 hybridoma cells. Anti-idiotypic antibody 3H1
CC elicits a specific immune response to a unique epitope of
CC carcinoembryonic antigen (CEA) that is not present on other
CC members of the CEA family or on normal adult tissues. 3H1
CC can be used as a vaccine to elicit immune responses in patients
CC with advanced CEA-associated disease or, when labeled, to enhance
CC tumour detection in imaging.
SQ Sequence 462 BP; 106 A; 124 C; 117 G; 115 T;

Query Match 76.1%; Score 265; DB 22; Length 462;
Best Local Similarity 90.0%; Pred. No. 1,26e-165;
Matches 315; Conservative 0; Mismatches 32; Indels 3; Gaps 2;

Db 82 gtccagctgaacagctctgagcctgagctggtgaaagccttcaactgaatttc 141
      |||
Oy 365 GTGCAGCTGCAGGAGTGAAGCTGAGAGCTGTAAGCTGGAAGTTCAATGAAGATATCC 424
      |||
Db 142 tgcgaagctctgttactcaactcactgacctacacatgaactggtgaaagcagacat 201
      |||
Oy 425 TGCAGAGCTTCTGTTACTCTTACTCTGCGCACACATGAACCTGGGTGAAGACCAT 484
      |||
Db 202 ggaagagccttgagtggtgtggcgatataaccccttcagtggtgataactaagc 261
      |||
Oy 485 GGAAGAAGACCTTGAAGTGAATGAGCTTATTAATCTTACATGATGATTAATACAC 544
      |||
Db 262 cagaatctcagggcagggccacattactgtgacaggttaccagacagcctacatg 321
      |||
Oy 545 CAGAAGTTCAAGGGCAGGGCCACATTACTGTAAACAAGTGTCCAGACAGCTTACATG 604
      |||
Db 322 gagctcctcagctgacatctgagagctcgtcagctcattactgttcaattaccggt 381
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Oy 605 GAGCTCTCAGTGTGACATCTGAGGACTCTGCGAGTCTATTACTGTG-CA--AGGAGGTT 661
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Db 382 ccctactgtactcagatctctgaggcgagggaccagggctacacgctc 431
      |||
Oy 662 ACGAGCTGACTTTCATGTCTGGGCGCAGGAGCACACGCTCACCGTCTC 711

RESULT 5
ID T31541 standard; cDNA: 462 BP.
AC T31541;
DT 18-SEP-1996 (first entry)
DE 3H1 heavy chain variable region cDNA.
KM Anti-idiotypic monoclonal antibody; Mab; 3H1; CEA;
KW carcinoembryonic antigen; cancer; gene therapy; immunotherapy;
OS vaccine; genetic immunisation; heavy chain; VH; ss.
Mus sp.
FH Key Location/Qualifiers
FT cds 22..462
      /tag= a
      /product= 3H1 heavy chain variable region
PI WO9620277-A2.
PN 04-JUL-1996.
PF 28-DEC-1995; U17103.
PR 28-DEC-1994; US-365484.
PA (KENT ) UNIV KENTUCKY.
PI Chatterjee M, Chatterjee SK, Foon KA, Kohler H;
DR WPI: 96-321850/32.
DR P-PSDB: R98411.
PT Recombinant monoclonal anti-idiotypic antibody 3H1 sequences - used
PT to develop prods. for the detection and treatment of
PT carcinoembryonic antigen-associated diseases, partic. cancers
PS Claim 6: Fig 2A: 121pp; English.
CC A cDNA clone (T31541) codes for the heavy chain variable region
CC (VH) (R98411) of 3H1, a murine monoclonal anti-idiotypic antibody
CC that mimics a specific epitope of the 180,000 mol.wt.
CC carcinoembryonic antigen (CEA) and which elicits an immune response
CC in patients with advanced CEA-associated disease, e.g. colorectal
CC cancer. It was obt'd. by PCR amplification of 3H1 hybridoma DNA
CC (see also T31545-46). The isolated polynucleotide, and/or a
CC polynucleotide (see also T31540) coding for the VL region (R98410)
CC of 3H1 can be used to design probes and primers, in expression
CC systems, and in pharmaceutical applns., including vaccines, gene
CC therapy and genetic immunisation, partic. against cancer.
SQ Sequence 462 BP; 106 A; 124 C; 117 G; 115 T;

Query Match 76.1%; Score 265; DB 21; Length 462;
Best Local Similarity 90.0%; Pred. No. 1,26e-165;
Matches 315; Conservative 0; Mismatches 32; Indels 3; Gaps 2;

Db 82 gtccagctgaacagctctgagcctgagctggtgaaagccttcaactgaatttc 141
      |||
Oy 365 GTGCAGCTGCAGGAGTGAAGCTGAGAGCTGTAAGCTGGAAGTTCAATGAAGATATCC 424
      |||
Db 142 tgcgaagctctgttactcaactcactgacctacacatgaactggtgaaagcagacat 201
      |||
Oy 425 TGCAGAGCTTCTGTTACTCTTACTCTGCGCACACATGAACCTGGGTGAAGACCAT 484
      |||
Db 202 ggaagagccttgagtggtgtggcgatataaccccttcagtggtgataactaagc 261
      |||
Oy 485 GGAAGAAGACCTTGAAGTGAATGAGCTTATTAATCTTACATGATGATTAATACAC 544
      |||
Db 262 cagaatctcagggcagggccacattactgtgacaggttaccagacagcctacatg 321
      |||
Oy 545 CAGAAGTTCAAGGGCAGGGCCACATTACTGTAGACAAGTCGTCAGACAGGCTACATG 604
      |||
Db 322 gagctcctcagctgacatctgagagctcgtcagctcattactgttcaattaccggt 381
      |||
Oy 605 GAGCTCTCAGTGTGACATCTGAGGACTCTGCGAGTCTATTACTGTG-CA--AGGAGGTT 661
      |||
Db 382 ccctactgtactcagatctctgaggcgagggaccagggctacacgctc 431
      |||
Oy 662 ACGAGCTGACTTTCATGTCTGGGCGCAGGAGCACACGCTCACCGTCTC 711

RESULT 6
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OS Synthetic.
FH Key 11..1710 Location/Qualifiers
FT unsure /*tag= a
FT /note= "Sequence not given in the specification"
FT cds 1848..2552
FT /*tag= b
FT /note= "Chimeric 128.1 VH/CH1 region"
FT cds 2945..2980
FT /*tag= c
FT /note= "Undefined ORF1"
FT cds 3099..3425
FT /*tag= d
FT /note= "Undefined ORF2"
FT /*tag= e
FT /note= "Sequence not given in the specification"
FT /*tag= f
FT /note= "Sequence not given in the specification"
FT MOJ310819-A.
PN 10-JUN-1993.
PD 24-NOV-1992; U10206.
PR 26-NOV-1991; US-800458.
PA (ALKE-) ALKERMES INC.
PI F1000 PM:
DR WPI: 93-196742/24.
DR P-PSDB; R41707-09.
PT Antibody conjugates specific for transferrin receptor - used
PT for diagnosis and treatment of cancer, AIDS and neurological
PT disorders
PS Disclosure; Fig 17A-F; 151pp; English.
PS The sequences given in Q43846-48 represent the expression vectors
CC PAH4625, PAH4807 and PAH4808. These vectors represent the cloning
CC of the different human gamma isotypes, gamma-2, gamma-3 and gamma-4
CC respectively, with the variable region of the murine monoclonal
CC antibody 128.1. These plasmids each encode a chimeric monoclonal
CC antibody in which the heavy chain (VH) is derived from a murine
CC source and the sequences encoding CH1, CH2 and CH3 are derived from
CC a human source. These vectors in combination with the chimeric light
CC chain vector, PAH4611 (see also Q43845), were transfected into SP2/0
CC cells and clones were isolated. Antibody analysis using biosynthe-
CC tically labeled proteins, immunoprecipitation and SDS-PAGE indicated
CC appropriate bands for the heavy and light chains as well as the
CC assembled antibody for the gamma-3 and gamma-4 chimeras. No detectable
CC protein was isolated for the gamma-2 transfectants. 128.1 is an anti-
CC human transferrin receptor antibody which binds to the transferrin
CC receptor on brain capillary endothelial cells. This antibody may be
CC used in a conjugate in which it is linked to a neuropharmaceutical or
CC diagnostic agent. The conjugate may be used to treat or prevent
CC neurological disorders eg. brain tumours, AIDS, stroke, epilepsy,
CC Parkinsons and Alzheimers disease. It may also be used for diagnostic
CC methods.
SQ Sequence 10704 BP; 2125 A; 2189 C; 2130 G; 2031 T;
Query Match 73.9%; Score 257; DB 7; Length 10704;
Best Local Similarity 87.0%; Pred. No. 6.39e-160;
Matches 302; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

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QY 545 CAGAGTTCAGGCGCAAGGCCATTACTGTACAGACAGTCGTCACAGCAGCCTACATG 604
DB 2148 gaggctcctagcttcgacatcgtgagcactgtgacgttattactgtgcaagagctact 2207
QY 605 GAGCTCCTCAGCTGTGACATCTGAGCAGCTGCGAGTCTATTACTGTGTCAGAGGAGTTACG 664
DB 2208 tactattcttgacactcgtgggtcaaggaactcgtacgcgttc 2254
QY 665 GAGTGTACTTGTGATGTGTGGGCGAGGACCCAGTGCAGTCCCTTC 711

RESULT 9
ID Q43848 standard; DNA; 10844 BP.
AC Q43848;
DT 20-OCT-1993 (first entry)
DE Plasmid PAH4808.
KW Polymerase chain reaction; primer; PCR; amplify; murine; PAH4625;
KW heavy; light; chain; variable; constant; region; anti-human; PAH4807;
KW transferrin; receptor; antibody; brain; capillary; PAH4808; gamma-2;
KW endothelial cell; conjugate; neuropharmaceutical; gamma-3; gamma-4;
KW diagnostic; agent; tumour; AIDS; stroke; epilepsy; monoclonal;
KW Parkinsons disease; Alzheimers disease; SP2/0 cell; ss.
OS Synthetic.
FH Key Location/Qualifiers
FT unsure 2070..3769
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FT 3907..4611
FT /*tag= b
FT /note= "Murine 128.1 VH/human gamma-4 CH1"
FT cds 4999..5034
FT /*tag= c
FT /note= "Undefined ORF1"
FT cds 5153..5482
FT /*tag= d
FT /note= "Undefined ORF2"
FT cds 5580..5900
FT /*tag= e
FT /note= "Undefined ORF3"
FT unsure 6128..6329
FT /*tag= f
FT 6336..6635
FT /*tag= g

MOJ310819-A.
PN 10-JUN-1993.
PD 24-NOV-1992; U10206.
PR 26-NOV-1991; US-800458.
PA (ALKE-) ALKERMES INC.
PI F1000 PM:
DR WPI: 93-196742/24.
DR P-PSDB; R41715-18.
PT Antibody conjugates specific for transferrin receptor - used
PT for diagnosis and treatment of cancer, AIDS and neurological
PT disorders
PS Disclosure; Fig 19A-F; 151pp; English.
PS The sequences given in Q43846-48 represent the expression vectors
CC PAH4625, PAH4807 and PAH4808. These vectors represent the cloning
CC of the different human gamma isotypes, gamma-2, gamma-3 and gamma-4
CC respectively, with the variable region of the murine monoclonal
CC antibody 128.1. These plasmids each encode a chimeric monoclonal
CC antibody in which the heavy chain (VH) is derived from a murine
CC source and the sequences encoding CH1, CH2 and CH3 are derived from
CC a human source. These vectors in combination with the chimeric light
CC chain vector, PAH4611 (see also Q43845), were transfected into SP2/0
CC cells and clones were isolated. Antibody analysis using biosynthe-
CC tically labeled proteins, immunoprecipitation and SDS-PAGE indicated
CC appropriate bands for the heavy and light chains as well as the
CC assembled antibody for the gamma-3 and gamma-4 chimeras. No detectable
CC protein was isolated for the gamma-2 transfectants. 128.1 is an anti-
CC human transferrin receptor antibody which binds to the transferrin
CC receptor on brain capillary endothelial cells. This antibody may be
CC used in a conjugate in which it is linked to a neuropharmaceutical or
CC diagnostic agent. The conjugate may be used to treat or prevent
CC neurological disorders eg. brain tumours, AIDS, stroke, epilepsy,

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FH Key Location/Qualifiers
FT unsure 11..1710
FT /tag= a
FT cds 1848..2546
FT /tag= b
FT /note= "128.1 VH/human gamma-3 CH1"
FT cds 2939..2980
FT /tag= c
FT /note= "Undefined ORF1"
FT cds 3133..3177
FT /tag= d
FT /note= "Undefined ORF2"
FT cds 3672..4001
FT /tag= e
FT /note= "Undefined ORF3"
FT cds 4099..4419
FT /tag= f
FT /note= "Undefined ORF4"
FT unsure 4630..5559
FT /tag= g
FT unsure 5566..5864
FT /tag= h
FT unsure 6720..6744
FT /tag= i
PN WO9310819-A.
PD 10-JUN-1993.
PE 24-NOV-1992; 010206.
PR 26-NOV-1991; US-800458.
PA (ALKE-) ALKERMES INC.
PI Friden PM:
PI WPI: 93-196742/24.
DR P-PSDB; R41710-14.
PT Antibody conjugates specific for transferrin receptor - used
PT for diagnosis and treatment of cancer, AIDS and neurological
PT disorders
PS Disclosure: Fig 18A-F; 151pp; English.
CC The sequences given in Q43846-48 represent the expression vectors
CC PAH4625, PAH4807 and PAH4808. These vectors represent the cloning
CC of the different human gamma isotypes, gamma-2, gamma-3 and gamma-4
CC respectively, with the variable region of the murine monoclonal
CC antibody 128.1. These plasmids each encode a chimeric monoclonal
CC antibody in which the heavy chain (VH) is derived from a murine
CC source and the sequences encoding CH1, CH2 and CH3 are derived from
CC a human source. These vectors in combination with the chimeric light
CC chain vector, PAH4611 (see also Q43845), were transfected into SP2/0
CC cells and clones were isolated. Antibody analysis using biosynthe-
CC tically labelled proteins, immunoprecipitation and SDS-PAGE indicated
CC appropriate bands for the heavy and light chains as well as the
CC assembled antibody for the gamma-3 and gamma-4 chimeras. No detectable
CC protein was isolated for the gamma-2 transfectants. 128.1 is an anti-
CC human transferrin receptor antibody which binds to the transferrin
CC receptor on brain capillary endothelial cells. This antibody may be
CC used in a conjugate in which it is linked to a neuropharmaceutical or
CC diagnostic agent. The conjugate may be used to treat or prevent
CC neurological disorders eg. brain tumours, AIDS, stroke, epilepsy
CC Parkinsons and Alzheimers disease. It may also be used for diagnostic
CC methods.
SQ Sequence 12132 BP; 2292 A; 2441 C; 2285 G; 2156 T;

Query Match 73.9%; Score 257; DR 7; Length 12132;
Best Local Similarity 87.0%; Pred. No. 6.39e-160;
Matches 302; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

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QY 485 GGAAGAACCTTGAGTGATGACTTATTAATCCTTAACATGATGATTAAGTACAGC 544
DB 2088 cagaagttcaaggacaggcccttaactatgacaaagtcacacagcctacatg 2147
QY 545 CAGAAGTTCAAGGCGAAGGCCACATTACTGTAGACAAGTCTCCAGCAGACCTTACATG 604
DB 2148 gagctcctcagctcagacatctgagacatctgagctcctatctatctgcaagagcctacat 2207
QY 605 GAGCTCTTAGTGTGACATCTGAGACCTCTGCAGTCTATTACTGTGCAAGGAGGTTACG 664
DB 2208 tactattcttgactactcgtgggtcaaggaacctcagtcacagctc 2254
QY 665 GACTGCTACTTGATGTCTGGGCGGAGGAGCAGCAGTCAAGCTCTCTC 711

RESULT 12
ID Q45428 standard; CDNA; 443 BP.
AC Q45428;
DT 17-NOV-1994 (first entry)
DE KM-750 heavy chain.
KW Monoclonal antibody; Ab; ganglioside GM2; chimera;
KW chimeric antibody; expression vector; heavy; light; chain;
KW hypervariable region; CDR; constant region; hypriodoma;
KW Ig; immunoglobulin; KM-796; KM-750; KM-603; cancer; ss.
OS Mus musculus.
FH Key Location/Qualifiers
FT cds 33..443
FT /tag= a
FT /note= "excluding stop codon"
FT signal_peptide 33..89
FT /tag= b
FT /note= "Sig-peptide"
FT misc_feature 180..194
FT /tag= c
FT /note= "hypervariable region 1"
FT misc_feature 252..287
FT /tag= d
FT /note= "hypervariable region 2"
FT misc_feature 384..410
FT /tag= e
FT /note= "hypervariable region 3"
PN AD9346181-A.
PD 17-MAR-1994.
PR 07-SEP-1993; 046181.
PR 07-SEP-1992; JP-238452.
PA (KYOMA ) KYOMA HAKKO KOGYO KK.
PI Hanei N. Hasegawa M, Koike M, Kuwana Y, Nakamura K,
PI Shitara K.
PI WPI: 94-126857/16.
DR P-PSDB; R53330.
PT Humanised antibody specific for ganglioside GM2 - used for
PT producing a cytotoxic effect on cancers such as melanoma,
PT neuroblastoma and glioma.
PS Disclosure: Page 107-108; 191pp; English.
CC Chimeric human Ab expression vectors are constructed by inserting
CC the Ab heavy and light chain variable region-encoding CDNA
CC isolated from hybridomas producing a mouse or rat monoclonal Ab
CC reacting with the ganglioside GM2 respectively into an expression
CC vector for use in animal cells which contains the human Ab heavy and
CC light chain constant region-encoding CDNA. The expression vectors
CC are introduced into animal cells and the transformant thus obtained
CC is cultured for the prodn. of a chimeric human Ab reacting with the
CC ganglioside GM2. In contrast to mouse monoclonal Abs, the chimeric
CC human Abs will not cause anti-mouse Ig Ab prodn. in the patient's
CC body but show a prolonged blood half-life, with a reduced frequency
CC of adverse effects, so that it can be expected to be superior
CC to mouse monoclonal Abs in the efficacy in the treatment of human
CC cancer, for instance.
CC Mouse anti-GM2 monoclonal Ab KM-796 and KM-750 and rat KM-603
CC heavy and light chain sequences are given in Q45426-30.
CC CDR regions for use in chimeric Abs are indicated in the
CC Features Table
SQ Sequence 443 BP; 109 A; 112 C; 119 G; 103 T;

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	Best Local Similarity	83.9%	Pred. No. 3,21e-154;		
	Matches 298;	Conservative	0;	Mismatches 49;	Indels 0;
				Gaps	0;
Db	93	gtccagctgcagcagctctgcagcctgcagctgtgtgaagctctggccttaagtgaaatatcc	152		
QY	365	gtgcagcgcgcgacgagctacgacacctgcagagctggtgaaccttgagagcttaattgaacattatcc	424		
Db	153	ttgcagagctcttgatatalacacatcactgcactacacacatgagcttggatgaaagcagagccat	212		
QY	425	tgcgaagactttctggttactctacttacttgcggccacacacatgaactgggtgaagcagagccat	484		
Db	213	ggaaagagcccttggatgtatgatatattatcttaacatggtgtgtactgcttaaac	272		
QY	485	ggaaagaaaccttgatggatggattggaccttatattatcttaacatgggtgtgtacttacttaaac	544		
Db	273	cagaagctcaagagcaagagccacacttgactctgacagagctccctccacacagacctacatg	332		
QY	545	cagaagttcaagggcagggcagggccacatttactgtatgacaaagtctgcagacacagccttaccatg	604		
Db	333	gaagctccacagccttgacacatctgagagactctgcagcttatacttactgtgcaagacgaggagag	392		
QY	605	gagcttccctcactgacttgacatctgaaagaaacttgcacgtctattactgctgcaaaagagggattacg	664		
Db	393	tattactcagagcctgagagctgagggcgaagggactctgtctactgtctc	439		
QY	665	gacttgcgtacttccatgattgcttgggggcgcaggggacacacggctcaccgctct	711		

DB	Seq	Query Match	Best Local Similarity	Matches	Conservative	Score	DB	Length	Indels	Gaps
13	gtcgaagcttcgtgtactcattactcgtgctacttatgaaacttggtgatacgaagcattc	70.48	85.98	293	0	245	5	356	0	0
365	gttcgaagcttcgtgtactcattactcgtgctacttatgaaacttggtgatacgaagcattc	70.48	85.98	293	0	245	5	356	0	0
73	gttcgaagcttcgtgtactcattactcgtgctacttatgaaacttggtgatacgaagcattc	70.48	85.98	293	0	245	5	356	0	0

QY	425	TGCAAGACTTGTGGTTACTACTATTACAGTGGCCACACACATGAACCTGGGTGAAGCAGAGCCAT	485
Db	133	ggaaagagcctttagtggtgatttgagcgtattaaaccttaacatggtgatacttctacaac	192
QY	485	GGAAAGAACCTTGATGGATGGATGGACTTATTATTCCTTACATAGTGTGATTACTACTAACAC	544
Db	193	cagaattccaaggccaaggccacattactctagaacaatccctctagaagcccacatg	255
QY	545	CAGAAGTTCAAGGGCCAAAGGCCACACTTACTCTTAACAAGTCGTCCACACAGCCTTAATG	604
Db	253	gaactccggagccttgacatcttgaaagactctgcattatctattttgtcaagaaggggggtc	312
QY	605	GAGCTCCCACTCTGCAATCTGAGATCTGAGAGCACTCTGCACTCTTACTCTGTCGAAGAGGGTTACG	664
Db	313	acgacgaggtttgttactgtagtgcgtccacggggaacccaggttcac	353
QY	665	GACTGTACTTTCGATGTCTGGGGCGCAGGGGCCACCGGTTCAC	705

RESULT	14
ID	T86309 standard; DNA; 717 BP.
AC	T86309;
DE	06-APR-1998 (first entry)
D	Single chain anti-disialoganglioside GD2 antibody 5F11-scFv.
KW	Antibody construct; disialoganglioside; GD2; single chain Fv fragment;
KW	scFv; tumour; neuroblastoma; osteosarcoma; soft tissue sarcoma;
KW	tissue imaging; target delivery; toxin; streptavidin;
KW	pro-drug converting enzyme; GD2-targeted lymphocyte; ss.
OS	Synthetic.
PN	M09734634-A1.
PD	25-SEP-1997.
PF	20-MAR-1997; U04427.
PR	20-MAR-1996; US-013703.
PA	(SLOAN) SLOAN KETTERING INST CANCER RES.
PI	Cheung NY, Guo H, Larson SM, Rivlin K, Sadelaar M;
DR	WPI: 97-479996/44.
PT	Recombinant single chain anti-disialoganglioside GD2 antibody -
PT	useful to detect tumour cells expressing GD2 and to target
PT	therapeutic agents, e.g. toxins, to such cells
PS	Disclosure; Page 11; 31pp; English.
CC	The present sequence encodes a recombinant single chain peptide,
CC	5F11-scFv. The peptide is an antibody construct comprising the variable
CC	regions of the heavy and light chains of an antibody against
CC	disialoganglioside (GD2) as a single chain Fv fragment (scFv). GD2 occurs
CC	in many tumour types including neuroblastoma, osteosarcomas and other
CC	soft tissue sarcomas, medulloblastomas, high grade astrocytomas,
CC	melanomas and small cell lung cancer. The peptide can be detectably
CC	labelled, preferably with 99m-Tc, for tissue imaging of cells expressing
CC	GD2. It can also be used to target delivery of a therapeutic or
CC	pre-therapeutic agent, such as a toxin, streptavidin or a pro-drug
CC	converting enzyme, to cells expressing GD2. The peptide may further
CC	comprise CDB to facilitate the formation of GD2-targeted lymphocytes.
CC	T cells containing the peptide can also be used to target GD2-producing
CC	tumour cells.
SQ	Sequence 717 BP: 180 A; 181 C; 195 G; 159 T;
<hr/>	
Query Match	69.5%; Score 242; DB 37; Length 717;
Best Local Similarity	86.7%; Pred. No. 3,106-149;
Matches 301; Conservative	0; Mismatches 43; Indels 3; Gaps 2;
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D	4 gtgaactgcagcgacgtcaaggacctgaactgctgtgaaacctggcgcttcagtlaaatatcc 63
Y	
Q	365 gTGCAGCTGAGAGATCACGAGACTTCAGGGTGGAAGCGCTGGAGGTTCAATGAAATATCC 424
D	64 tgcgaactctcgganacaataattcacgtgaatacaccatgatcactgggttgaaagcagaccat 123
Y	
Q	425 TGCGAACATCTTGATTACCATTCATTCAGTGCACCACACATGAAGTAATGGGTGAACACAACGCCAT 484
D	124 ggagaagaagccttaagttgatttgtagtgtttaatacctaacaatggtgtgactaacataaag 183
Y	
O	485 GGAAAGAACCTTAGTGAGATGGACTTATATATCTTCAATATGGTGATACACTAATCAAC 544
D	184 cagaagtccaagggcacaagcccacattgactgtgaagcaagctctccagaacagcctaccatg 243


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/noce="Organ: mammary gland; Vector: pT73D-Pac
(Pharmac) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer [5,
TGTACCAATCTGAAGTGGAGCGCCGCAAGTGTGTGTGTGTGTGTGT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmac), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M.Fatima
Bonaldo.
/db_xref="taxon:10090"
/clone_11b="Soares mouse mammary gland NbMwC"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
BASE COUNT      80 a      67 t      1 others
ORIGIN
      230
Query Match      46.0%      Score 160; DB 18; Length 310;
Best Local Similarity 79.3%;      Pred. No 9,99e-268;
Matches      230;      Conservative      0;      Mismatches 58;      Indels      2;      Gaps      2;

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LOCUS	2	294 bp	mRNA	EST	12-JUN-1998
DEFINITION	u873604.1	Soares 2NbMT	Mus musculus cDNA clone 1363158.5'	similar to gb:M18512 IG HEAVY CHAIN PRECURSOR V-I REGION (HUMAN); gb:M12376	
REFERENCE				Mouse immunoglobulin H-chain V-region pseudogene mRNA, complete (MUSE); mRNA sequence.	
ACCESSION				AI007196	
NID				93216735	
KEYWORDS				EST.	
SOURCE				house mouse.	
ORGANISM				Mus musculus	
REFERENCE				Eukaryotes: Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
AUTHORS				1 (bases 1 to 294)	
				Maria,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisler,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Stepien,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.	
TITLE				The Washu-HMT Mouse EST Project	
JOURNAL				Unpublished (1996)	
COMMENT				Contact: Maria M/Mouse EST Project Washu-HMT Mouse EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800	

Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MOI:896378
Trace considered overall poor quality
Seq primer: -28ml3 rev2 RT from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1..294
source

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/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5].
TGTGACCAATCTGATGAGTGGGAGCGCCGCTTTTCTTTTCTTTTCTTTT
3'"]; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. RNA
provided by Dr. Bertrand Jordan. Library went through two
rounds of normalization, and was constructed by Bento
Soares and M. Fatima Bonaldo."
/db_xref="taxon:10090"
/clone_1fb="Soares 2NDMT"
/clone_1fb="1363158"
/sex="male"
/tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"

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Query Match	42.08%	Score 146;	Db 15;	Length 294;
Best Local Similarity	76.7%;	Pred. No. 1,51e-256;		
Matches 224;	Conservative 0;	Mismatches 66;	Indels 2;	Gaps 2;
Db 2	GTCCAACTGACAGCAGCCCTGGGGCTGAGCATTGGTGAGAGACTGGGCTTTCAGTAGAGCTGTA	61		
Query 365	GTGCGAGCTGACGAGATGAGGACCTGAGG-TGGTGAAGCCTGGAAGTTTCATGAGATATAC	423		
Db 62	CTGCAAGGATTTACAGGCTACACACTTACACCACCTACTGGATGGATGGGTGAAGCAGAGGCA	121		
Query 424	CTGCAAGACTCTGGTTACATTCATTCACCTAGGACCACACCATCAACAGGGGTGAAGCAGAGCCA	483		
Db 122	TATACAAGGCTGATGATGATGATGTTAGTACATTGAGCCCTTCAGATATGATGAGACTCCATCA	181		
Query 484	TGGAAAGAACCTTGATGATGGATTTGAGACTTATTAATCTTACAAATGGTATATCTACTACAA	543		
Db 182	TCAAAAGTTCAAGGACCAAGGCCACACATTGACTGTAGACAAATTCACGACAGAGCCTACAG	241		
Query 544	CCAGAACTTCAAGGGCAAGGCCACACATTACTGTAGACAAATGTCGCCAGACAGCCTACA-602			
Db 242	TGCAGCTCAGCAGACATGACATCTGAGGACTCTGGCGTCTTACTGTGCAG-293			
Query 603	TGGAGCTCTCCAGTCTGACATCTGAGGACTCTGCAGTCTTACTGTGCAG-654			
RESULT 3				
LOCUS	AA569186	387 bp	mrna	EST
DEFINITION	nm3010.0.s1 NCI-CGAP_L1P2 Homo sapiens cDNA clone IMAGE:1061683			
	similar to gb:U02325 IG HEAVY CHAIN PRECURSOR V-1 REGION (HUMAN),			
ACCESSION	AA569186			
NID	G2342240			
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;			
	Primates; Catarrhini; Hominoidea; Homo.			
REFERENCE	1 (bases 1 to 387)			
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .			
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),			
	Tumor Gene Index			

ACCESSION	AA291381
NID	01939359
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS	1 (bases 1 to 379) Hallier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Maier,M., Parsons,D., Rifkin,L., Rohlfing,T., Tan,F., Trevasakis,E., Westerton,R., Williamson,A., Woldmann,P. and Wilson,R.
TITLE	Mashu-Merck EST Project
JOURNAL	Unpublished (1995)
COMMENT	Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@wuston.wustl.edu This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1576 Std Error: 0.00 Seq primer: -28ml3 rev2 EF from Amersham High quality sequence stop: 361. Location/Qualifiers 1..379 /organism="Homo sapiens" /note="Organ: ovary; Vector: pT73D (Pharmacia) with a modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer TGTACCAATCTGAAGTGGAGGCGGCGGCTTTTCTTTTCTTTT 37 double-stranded cDNA was size selected, ligated to Eco I adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Patima Ronaldo." /db_xref="taxon:9606" /clone_id="725234" /sex="Female" /issue_type="ovarian tumor" /lab_host="DH10B (ampicillin resistant)" <1..>379
FEATURES	
SOURCE	
BASE COUNT	85 a 82 c 121 g 91 t
ORIGIN	
Query Match	23.6%; Score 82; DB 8; Length 379;
Best Local Similarity	65.9%; Pred. No. 1,106-117;
Matches	191; Conservative 0; Mismatch 97; Indels 2; Gaps 2
Db	37 GTTAGTTGGTGCAGTGTGACCTGAGGTGAAGAC-TGG-GGCCAGTGAGGCTCC 94
Qy	365 GTGACGCTGCAGGATCGACCTGAGAGTGTGAAGCCTGGAGGTTCAATGAATATCC 424
Db	95 TGTAAAGCCTTGGTACACCTTTGGACCTTTTGGTATCACTGGGTGGCGGAGCCCT 154
Qy	425 TGCAGACTTTGGTATCTACTTACTGCGCACACCACTGAAGCTGGTGAAACAGCCAT 484
Db	155 GGACAGAGGCTTGAATGATGGATGATCGATCGCTTTTCAATGTTAGACAAATTTGCA 214
Qy	485 GGAAGAACCTTGATGATGATGGAATTAATTCCTTCAATGATGATACATACATACAC 544
Db	215 GGGAGTTTTCAGGACAGATGAGCTTGACACCTAACAATCCAGAAATACAGCTTACATG 274
Qy	545 CAGAAGTTCAAGGGCAGGCGCACATTTTACTGTAGACAAGTGTCCACACAGCCTACATG 604
Db	275 GAGCTAGGAACCTGAGATCTGAGACACAGCCGCAATATATTTCTGTGGAG 324
Qy	605 GAGCTCTCACTGTGACATCTGAGAGACTGTCAAGTCTTATTACTGTGCAAG 654

LOCUS	6	T28938	209 bp	MRNA	EST	06-SEP-1995
DEFINITION	EST61186 Homo sapiens cDNA 5' end similar to immunoglobulin mu heavy chain, VDJ regions (GB:M1751) (Hr:3055).					
ACCESSION	T28938					
NID	9611036					
KEYWORDS	EST.					
SOURCE	human primer-M13 Reverse Library-Human White blood cells.					
ORGANISM	Homo sapiens					
REFERENCE	<p>Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Felder,R.A., Bult,C.U., Lee,N., Kitzness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Chui,M.-W., Clayton,R.A., Cline,R.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.M., Glodak,A., Gnehm,C.L., Hanns,M.C., Hedblom,E., Hinkle,J.P.S., Kelley,J.M., Kirekh,K.M., Kelley,J.C., Liu,L.-T., Marmaro,S.M., Merrick,J.M., Moreno-Palanges,R.F., McDonald,L.A., Nguyen,D.T., Pellegrini,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bedark,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.-J., Dimke,D., Feng,P., Ferrie,A., Fischer,C., Hastings,G.A., He,W.-W., Hu,Y.-S., Greene,J.M., Gruber,J., Hudson,P., Kim,A., Kozak,D.L., Kunsch,C., Ji,H., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Ming,J., Xu,C., Yu,G.-L., Ruben,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A., Resettine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.</p> <p>Initial Assessment of Human Gene Diversity and Expression Pattern Based Upon 52 Million Basepairs of cDNA Sequence</p> <p>Unpublished (1995)</p>					
TITLE						
JOURNAL						
COMMENT	<p>Contact: Venter, J.C. The Institute for Genomic Research 932 Clopper Rd. Gaithersburg, MD 20878 Tel: 3018698056 Fax: 3018699423</p> <p>Email: tdbinfo@tdb.tigr.org For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Databases (tdbinfo@tdb.tigr.org).</p> <p>location/Qualifiers</p> <p>1..209</p> <p>organism="Homo sapiens"</p> <p>mrna</p> <p>BASE COUNT</p> <p><1..>209</p> <p>43 a 62 c 48 g 55 t 1 others</p> <p>ORIGIN</p>					
FEATURES	<p>source</p> <p>1..209</p> <p>location/Qualifiers</p>					
Query Match	23.3%; Score 81; DB 16; Length 209;					
Best Local Similarity	71.7%; Pred. No. 1,37e-115;					
Matches	134; Conservative 0; Mismatches 53; Indels 0; Gaps 0;					
Db	15 GTATGAGACTCGCCCTGGAAGCTTCGTAATATTTGTGTACATGCCAGGTTG 74					
Cp	573 GTAATGTGGCTTGGCCCTTGAACTTGTGTTGTAGTATACCATTCATGTAAGATTA 514					
Db	75 ATCCATCCATCCATCAAGCCTTTGTCCGGGGGCGTGGCCACCAATGATAGCATAG 134					
Cp	513 ATATGTCATATCCATCCATCAAGTCTTCTTCATGCGTCTTCACCCAGTTCATGATG 454					
Db	135 CTATGAGAGGTATCCAGAAAGCCTTGACAGAAACCTTACTAGAGGCCCGAGCTTCTTC 194					
Cp	453 CCAATGATAGTGTAACCAAGAGTCTTGACAGATATCTTCAATTAACCTCCAGGCTTACC 394					
Db	195 ACCTCAG 201					
Cp	393 ACCTCAG 387					

RESULT 7
LOCUS A116236 116 bp mRNA EST 02-SEP-1998
DEFINITION uc18608.t1 Soares mouse mammary gland NbMWG Mus musculus cDNA clone
1398374.5' similar to gb:M87789 IG GAMMA-1 CHAIN C REGION (HUMAN);
gb:X67210 M.musculus rearranged immunoglobulin gamma 2b heavy
(MOUSE); mRNA sequence.
ACCESSION A116236
NID 93516560
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota: Metazoa: Chordata: Vertebrata: Mammalia: Eutheria:
Rodentia: Sciurognathi: Muridae: Murinae: Mus.
AUTHORS 1 (bases 1 to 116)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:910090
Trace considered overall poor quality
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1. 116
/organism="Mus musculus"
/strain="C57BL/6J"
/note="Organ: mammary gland; Vector: pT73D-Pac
(Pharmacia) with a modified polylinker; Site.1: Not I;
Site.2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer [5'
TGTTACCAATCTGAGTGGAGGAGCGCCGCAATGTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M.Fatima
Bonaldo.
/db_xref="taxon:10090"
/clone="1398374"
/clone_lib="Soares mouse mammary gland NbMWG"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
BASE COUNT 38 a 32 c 25 g 21 t
ORIGIN
Query Match 22.7%; Score 79; DB 17; Length 116;
Best Local Similarity 86.2%; Pred. No. 2,066-111;
Matches 94; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

RESULT 8
LOCUS AA710970 431 bp mRNA EST 24-DEC-1997
DEFINITION vt93h09.t1 Soares mouse mammary gland NbMWG Mus musculus cDNA clone
1178753.5' similar to gb:M18512 IG HEAVY CHAIN PRECURSOR V-I REGION
(HUMAN); gb:X70423 M.musculus mRNA for monoclonal antibody heavy
chain gamma (MOUSE); mRNA sequence.
ACCESSION AA710970
NID 92720888
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota: Metazoa: Chordata: Vertebrata: Mammalia: Eutheria:
Rodentia: Sciurognathi: Muridae: Murinae: Mus.
AUTHORS 1 (bases 1 to 431)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:936601
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 198.
Location/Qualifiers
1. 431
/organism="Mus musculus"
/strain="C57BL/6J"
/note="Organ: mammary gland; Vector: pT73D-Pac
(Pharmacia) with a modified polylinker; Site.1: Not I;
Site.2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer [5'
TGTTACCAATCTGAGTGGAGGAGCGCCGCAATGTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M.Fatima
Bonaldo.
/db_xref="taxon:10090"
/clone="1178753"
/clone_lib="Soares mouse mammary gland NbMWG"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
BASE COUNT 112 a 103 c 112 g 104 t
ORIGIN

Query Match 21.8%; Score 76; DB 11; Length 431;
Best Local Similarity 63.9%; Pred. No. 3,386-105;
Matches 175; Conservative 0; Mismatches 99; Indels 0; Gaps 0;
Db 124 AGTGTGACCTGAGCTGAGAGGCTGAGAGAGCAGATCTCTGCAAGGCTTCTG 183
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 378 AGTAGAGACCTGAGAGTGTGAAGCTTGAGGCTTCAATGAAGATATCTGCAAGACTTCTG 437
Db 184 GGTATACCTTCACAACTATGATGAGCTGGGTGGAAGAACCTCCAGAAAGGTTTAA 243
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 438 GTTACTATCTACCTGAGCAACACATGAGTGGTGAAGCAGAGCCATGAAAGAACCTTG 497
Db 244 AGTGTGAGGCTGATTAACACCTACTCTGTGAGTGGCCAAATATGCTGATGACTTCAAG 303
||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 498 AGTGAATGACCTATATATACCTTACATGTGTATCTACTACACACAGAGTTCAAG 557

Db 304 GACGGTTGCTCTCTTTGGAACCTCTGCACACTGCTATTTGCAGATCAACAAC 363

QY 558 GCAAGGCCATTTACTTGTGTACAGACAGTGTCCACAGCAGCTTACATGAGCTCTCTCAGTC 617

Db 364 TCAAAATGAGAGCAGCGCTACATATTTCTGTC 397

QY 618 TGACATCTGAGAGCTGTGACGTCTATTACTGTCTG 651

RESULT 9

LOCUS 275609 287 bp mRNA EST 06-SEP-1995

DEFINITION EST101034 Homo sapiens cDNA 5' end similar to immunoglobulin mu heavy chain, VDJC regions (GB:MI8512) (HT:3056).

ACCESSION 275609

NID 9609707

KEYWORDS EST.

SOURCE human primer-MJ3 Reverse library-Human Pancreas.

ORGANISM Homo sapiens

REFERENCE Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 287)

ADAMS,M.D., Kervilavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bull,C.D., Lee,N., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Chiu,M.-W., Clayton,R.A., Cline,R.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,M.M., Fritchman,J.L., Georghagen,N.S.M., Gilek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,J.P.S., Kelley,J.M., Kimek,K.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palanges,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Uterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.-J., Dinke,D., Feng,P., Ferric,A., Fischer,C., Hastings,G.A., He,W.-W., Hu,J.-S., Greene,J.M., Gruber,D., Hudson,P., Kim,A., Kozak,D.L., Kunsch,C., Li,H., Meisner,P.S., Olsen,H., Raymond,L., Wei,Y.-F., Wing,J., Xu,C., Yu,G.-L., Ruben,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C. Initial Assessment of Human Gene Diversity and Expression Patterns based upon 52 Million Basepairs of cDNA Sequence unpublished (1995)

JOURNAL

TITLE

COMMENT

CONTACT: Venter, J.C.
The Institute for Genomic Research
932 Clopper Rd.
Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@db.tigr.org
For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database (tdbinfo@db.tigr.org)

FEATURES

source

1..287

location/Qualifiers

ORIGIN

mRNA

BASE COUNT 62 a 77 c 85 g 60 t 3 others

Query Match 20.4%; Score 71; DB 16; Length 287;
Best Local Similarity 70.3%; Pred. No. 7.44e-95;
Matches 123; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

Db 74 GTGCACTGTGTCAGTGTGGGCTGAGTGAAGAGCCTGGGCTCAGTGAAGGTCTCC 133

QY 365 GTGCACTGTGTCAGTGTGGGCTGAGTGAAGAGCCTGGGCTCAGTGAAGGTCTCC 424

Db 134 TGCAGACTTGTGATACGCTTCAAGCACTACTATATACAGTGTGATTCAGAGGCCCT 193

QY 425 TGCAGACTTGTGATACGCTTCAAGCACTACTATATACAGTGTGATTCAGAGGCCCT 484

Db 194 GGACAAAGGCTTGATGATGGGATGATGAACCTTCGACGTGTGTCACCAACT 248

QY 485 GGAAGAACCTTGATGATGGGATGATGAACCTTCGACGTGTGTCACCAACT 539

RESULT 10

LOCUS AA987559 336 bp mRNA EST 23-JUL-1998

DEFINITION OR83901.s1 NCI-CGAP Lu5 Homo sapiens cDNA clone IMAGE:1602480 3' similar to gb:M87789 IG GAMMA-1 CHAIN C REGION (HUMAN);, mRNA sequence.

ACCESSION AA987559

NID G3172923

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 336)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT

CONTACT: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html

Insert Length: 801 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 322.
Location/Qualifiers

1..336

location/Qualifiers

ORIGIN

BASE COUNT 82 a 86 c 100 g 68 t

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Best Local Similarity 61.7%; Pred. No. 1.02e-88;
Matches 179; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

Db 32 GTCCAGATGACAGTCAGAGGCTGAGTGAAGAACCCAGGCTCTTGGTGAAGTCAAC 91

QY 365 GTCCAGCTGAGAGATCAGAGACTGAGTGTGAAGCCCTGAGGTTCAATGAAGATATCC 424

Db 92 TGTCTTCCCTCTGAGAGCACTTTCGTTAGTGTGACTGTGACTGGGTGCAAGGCCCT 151

QY 425 TGCAGACTTGTGTTACTTCACTGATCCACACCATCATGAGTGTGTAAGCAGCCAT 484

Db 152 GGAACAAGGCGCTGAGTGAATGGGAATCATCCCATGCGTCATTACAGCAAGTACGA 211

QY 485 GGAACAAGGCGCTGAGTGAATGGGAATCATCCCATGAGTGAATGATTAATCACTAC 544

```

Db      101 CAGCTGGTCGACGTCCGAGGATGAAGAGCGCTGGCGCCTCAANTAAAGTCTCCGC 160
        ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy      368 CAGCTCAGAGGATCAGGACCTGAGGTGTGAAGCGCTGAGGTTCAATAGAATATCTCGC 427
        ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      161 AAGANNTCTGGTTACCCTTTACCAACAACCGATTACACTGGTGCGACAGGCCCTTGA 220
        ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy      428 AAGACTTCTGGTTACTCATTCATCTAGCGCCACACACATGAACTGGGTGAACAGAGCCATGA 487
        ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      221 CAAGGCGTCGAGTGCATGGATGCATCACCGCGTTACAATGCT 262
        - ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy      488 AAGAACCTTGAGTGGATGTGACTTATTTATCTTACAAATGCT 529
        ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT   12
LOCUS    AA377074      291 bp      mRNA
DEFINITION EST89603 Small intestine I Homo sapiens cDNA 5' end similar to
           similar to immunoglobulin heavy chain, VDJ regions (GB:214165),
           mRNA sequence.
ACCESSION
MID       AA377074
KEYWORDS  G2029413
SOURCE    EST.
ORGANISM  human.
REFERENCE
AUTHORS   Homo sapiens
           Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
           Vertebrata; Mammalia; Eutheria; Primates; Carnivora; Homidae;
           Homo.
           1 (bases 1 to 291)
ADAMS,M.D., Kerlavage,A.R., Fleischmann,R.D., Feldner,R.A.,
Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Val,C.,
Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
Fitzgerald,L.M., Fitzhugh,W.M., Frichman,J.L., Geopfangen,N.S.,
Gloddey,A., Ghem,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.,J.M.,
Kelley,J.M., Kelley,J.C., Liu,L.T., Marmaros,S.M., Merrick,J.M.,
Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Saudak,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Uterback,T.R., Weldon,J.P., Li,Y.,
Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dinke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
Kozak,D.L., Kunsch,C., Hungnig,J., Li,H., Weissner,P.S., Olsen,H.,
Raymond,L., Wei,Y.F., Wang,J., Xu,C., Yu,G.L., Ruben,S.M.,
Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
Fraser,C.M. and Venter,J.C.
Initial assessment of human gene diversity and expression patterns
based upon 85 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl.), 3-174 (1995)
96026280

TITLE     Contact: Kerlavage, AR
JOURNAL   Bioinformatics
MEDLINE   The Institute for Genomic Research
COMMENT   9712 Medical Center Drive, Rockville, MD 20850 USA
           Tel: 3018699056
           Fax: 3018699423
           Email: arkerlav@tigr.org
           For clone availability, additional sequence and expression
           information related to this EST, please check the TIGR Human Gene
           Index (http://www.tigr.org/tdb/hgi/hgi.html)
           Seq primer: M13 Reverse.

FEATURES
Source    Location/Qualifiers
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           /organism="Homo sapiens"
           /note=Organ: small intestine; Vector: pBluescript SK-;
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           /db_xref="ATCC:181500"
           /db_xref="taxon:9606"
           /clone_lib="Small intestine I"
           /dev_stage="adult"
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BASE COUNT
ORIGIN

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Best Local Similarity	66.0%	Pred. No. 1.19e-84		
Matches 134	Conservative 0	Mismatches 65	Indels 0	Gaps 0
Db	75	GTGCAGCTGTGTCATCTGGCGGCTGAGGTGAAGAGACCTCGGCTCTCTGTGTGAAGTTCG	134	
Oy	365	GTGCAGCTGCGAGGAGTGTGAGGAGCTGAGGTGGTGAACCTTGGAGGTTCAATGAAGATATCC	424	
Db	135	TGCAAGGCTATGGATTCACCTTCACTGATTTATCTATCAACTGGGTGCGAGGCCCTT	194	
Oy	425	TGCAAGACTTCTGGTATTCATTCCTCACTGGCGCAACCATCAATCGGTGAAGCAGGCAAT	484	
Db	195	GGACAGGAGCTATGATGGATGGATGAACCCAGCAATGGAGGCTCCGACATGCA	254	
Oy	485	GGAAAGAACTTGTAGTGTGATTCGATTCATTATTCCTTACATGTGTACTACTACTACAC	544	
Db	255	CAGAAGTTTCGGGGGAGAGCTAC	277	
Oy	545	CAGAAGTTTCAAGGCGCAGGCCAC	567	
RESULT	13			
LOCUS	AA948436	488 bp	mRNA	EST
DEFINITION	0n67801.s1 Soares-NFL-T.GBC.S1 Homo sapiens cDNA clone			23-JUN-1998
IMAGE	1561704.3'	similar to gb:M8512 IG HEAVY CHAIN PRECURSOR V-I-1		
REGION (HUMAN):		mRNA sequence.		
ACCESSION	AA948436			
NID	g3109689			
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;			
	Primates; Catarrhini; Hominoidea; Homo.			
REFERENCE	1 (bases 1 to 488)			
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .			
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),			
JOURNAL	Tumor Gene Index			
COMMENT	Unpublished (1997)			
	Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert_Strausberg@nih.gov This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert length: 1240 Std Error: 0.00 Seq primer: -40m13 fwd. ET from Amersham High quality sequence stop: 148.			
FEATURES	Location/Qualifiers			
SOURCE	1. 488			
	/organism="Homo sapiens"			
	/note="Organ: pooled; Vector: pFT73D-Pac (Pharmacia) with a modified polylinker; Site.1: Not I; Site.2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI-CGAP GC81) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo." /db_xref="taxon:9606"			
	/clone="IMAGE:1561704"			
	/clone_1lb="Soares-NFL-T.GBC-s1"			
	/lab_host="DH10B"			
BASE COUNT	108 a	88 g	181 t	
ORIGIN	111 c			
Query Match	18.4%	Score 64	DB 15	Length 488
Best Local Similarity	71.4%	Pred. No. 1.32e-80		
Matches 115	Conservative 0	Mismatches 45	Indels 1	Gaps 1

Df	271	CTGCACAGTAATACAGGCCCATGTCTCAGACTTACAGGCTGTCTAGCTCCCTGAGGCT	330
Cp	654	CTTGACAGTAATVAGACTGCAGAGCTCTCAGATGTCAAGCTGAGGGAGTCATGTAGGCT	595
Df	331	GTTGCTACATGACAGCGTCCCTGGTTATGTACTCTCCCTGGAACCTTGTCATCATGT	390
Cp	534	GTCCTGACAGCACTTGCTTACAGTAATGTGGCTTCCCTTGACACTTCGTGTGTAGTTA	535
Df	391	GTTTACCATTGCCAGCATGATTCACCCA-TTCACTCAAG	430
Cp	534	GTATCACCATGTGATGATTAATAAGTCCATCACTCAAG	494
RESULT	14		
LOCUS	T29670	238 bp	mRNA
DEFINITION	ESTH9669 Homo sapiens cDNA 5' end similar to Immunoglobulin heavy chain v region (GB:X61012) (HT:3220).		
ACCESSION	T29670		
MID	g611768		
KEYWORDS	EST.		
SOURCE	human primer-MJ3 Reverse library-Human Small Intestine.		
ORGANISM	Homo sapiens		
REFERENCE	Adams,M.D., Kerlavage,A.R., Fleischman,R.D., Feldner,R.A., Bult,C.J., Lee,N., Kirkness,E.F., Wrenstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Chiu,M.-W., Clifton,R.A., Cline,R.T., Cotton,M.D., Earle-Hughes,J., FINE,L.D., Fitzgerald,L.M., FitzHugh,W.M., Fitchman,J.L., Geoghegan,N.S.M., Glodde,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle Jr,P.S., Kelley,J.M., Klinker,K.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palancas,R.F., McDonald,I.A., Nguyen,D.T., Pellegriano,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Sudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.-J., Dimke,D., Feng,P., Fertile,A., Fischer,C., Hastings,G.A., He,W.-W., Hu,J.-S., Greene,J.M., Gruber,J., Hudson,P., Kim,A., Kozak,D.L., Kunisch,C., Ji,H., L.H., Meisner,P.S., Olsen,H., Raymond,U., Wei,Y.-F., Wang,J., Xu,C., Yu,G.-L., Ruben,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A., Hasselbine,W.A., Fields,C., Fraser,C.M. and Venter,J.C. Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 52 Million Basepairs of cDNA Sequence Unpublished (1995)		
JOURNAL COMMENT	Contact: Venter, JC The Institute for Genomic Research 932 Clopper Rd, Gaithersburg, MD 20878 Tel: 3018699056 Fax: 3018699423 Email: tcdinfo@tigr.org For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database (tcdinfo@tigr.org).		
FEATURES	location/Qualifiers		
source	1..238		
mrna	"/organism="Homo sapiens"		
BASE COUNT	<1..>238		
ORIGIN	46 a 70 c 69 g 52 t 1 others		
Query Match	17.8% Score 62; DB 16; Length 238;		
Best Local Similarity	72.8%; P-Id. No. 1,39e-76;		
Matches	99; Conservative 0; Mismatches 37; Indels 0; Gaps 0;		
Df	103	GTTGACCTGGTGCAGCTGGAGCTGAGTGGAAGAAGCCGGGGCTCAGTAGAGCTTCC	162
Cp	365	GTCAGCTGCAGAGAGTCAGAGCACTTGAGGTGTGAAGCCCTGGAGGTTCAATGAAGATATCC	424
Df	163	TGCAAGGCTTCTGATTACACTTTTACCACTTACCGTATACGCTGGGTGCGACAGGCCCCCT	222

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OY 425 TGCAAGATTCTGTTACTCATCTCAGCCACACATGAGTGGTGAAGAGCCAT 484
DB 223 GGACAGGCGCTTGACT 238
OY 485 GGAAGAGACTTGACT 500

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RESULT 15
LOCUS AA754459 252 bp mRNA EST 20-JAN-1998
DEFINITION 97SN1787 Rice Immature Seed Lambda ZAPII CDNA Library Oryza sativa
CDNA clone 97SN1787, mRNA sequence.
ACCESSION AA754459
NID 92801165
KEYWORDS EST.
SOURCE rice.
ORGANISM Oryza sativa

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REFERENCE Eukaryotae: Viridiplantae; Charophyta/Embryophyta group;
AUTHORS Embryophyta: Tracheophyta; seed plants; Magnoliophyta: Liliopsida;
          Poales; Poaceae; Oryza.
          1 (bases 1 to 252)
          Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R., Moon,E.P.,
          Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y.,
          Lee,M.C. and Eun,M.Y.
          Large-scale Sequencing Analysis of ESTs from Rice Immature Seed
          Unpublished (1998)

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TITLE Contact: Eun M.Y.
JOURNAL Department of Cytoogenetics
          National Inst. of Agri. Sci. and Tech, RDA
          Suwon, Kyunggi-do, Korea
          Tel: 82 331 290 0301
          Fax: 82 331 290 0307
          Email: myeun@snu20.asi.re.kr
          Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
          University, Yongin, Korea. 449-728 bhnahm@loserver.myongji.ac.kr
          Seq primer: M13 Reverse Primer.
          Location/Qualifiers

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FEATURES
Source
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/cultivar="Milyang23"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI. Directional cDNA library inserted into lambda ZAPII
vector at 5' end with EcoRI and 3' end with Xho I site."
/db_xref="taxon:4530"
/clone_lib="97SN1787"
/clone_lib="Rice Immature Seed Lambda ZAPII CDNA Library"
/tissue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
BASE COUNT 5 a 21 c 12 g 35 t 179 others
ORIGIN

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Query Match 17.0%; Score 59; DB 12; Length 252;
Best Local Similarity 11.1%; Pred. No. 1,35e-70;
Matches 26; Conservative 120; Mismatches 86; Indels 3; Gaps 2;

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DB 21 TSYBCHGNBVWCVASHGNYMSVHNCBTRGTHCDCKNVMSMTMGTVMBVNSGDWHY 80
CP 691 TGGGCCCGACATGAGATGACATCGTACCTCTGCGACAGTATAGATGACAG 632
DB 81 BYBNTKVDVGNHTRCSRMBVTRMAHYHDYTCBBIYNNNDYHMHBBMYBRTGCTTWM 140
CP 631 GTCTCAGATGTGACAGAGAGAGCTCCATGTAGGCTGTGAGACACTTGCTACAGT 572
DB 141 CMBHNTKCTAGSGWHTSTNYDKSNTMGVTSYDKSMHGWCSBVBVYHTRKYSTTRAT 200
CP 571 AAATGTGGCTTGCCCTTGAACTCTGGTGTAGTAGTATACCATGTGTAAGATTAAT 512
DB 201 R-SYTCVRKYCVMMTKKV--VKRYHVVBGCBRTDSKCKTMMTNKHMTSTTD 252
CP 511 AAGTCAATCCACGTCAAGTCTTTCATGAGCTCTGCTTCAACCAAGTTCATGCTG 457

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Search completed: Sat Jan 9 15:33:13 1999
 Job time : 500 secs.

ORGANISM Mus sp.
Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Mus.
REFERENCE 1 (bases 1 to 711)
AUTHORS Batta,J.K., Kasprzyk,P.G., Bird,R.E., Pastan,I. and King,C.R.
TITLE Recombinant anti-erbB2 immunotoxins containing pseudomonas exotoxin
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89 (13), 5867-5871 (1992)
MEDLINE 9235198
REMARK Genbank staff at the National Library of Medicine created this
entry [NCBI g1bbsg108547] from the original journal article.
This sequence comes from Fig. 1.
FEATURES
source
1..711
/organism="Mus sp."
/db_xref="taxon:10095"
gene
1..711
/partial
/gene="anti-erbB2 immunotoxin antigen binding region"
1..711
/partial
/note="anti-erbB2 immunotoxin antigen binding region"
/note="This sequence comes from Fig. 1."
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KRWITTSVLASGVPARESGSGSTISLTVSVEEDATYTCQWMSKPTFGSGS
KLEIKSTSGSGSKSGKGVOLQESPEVVKPGSKIKCKTSGSTFHTNNWYKOS
HKNLEWGLINDYNGDITNYNOKFKGKATFTYDKSSSTAYMEILLSDSAYVCAR
RTDWYFDWAGATYTVS"
BASE COUNT 175 a 182 c 190 g 164 t
ORIGIN
Query Match 100.0%; Score 42; DB 31; Length 711;
Best Local Similarity 100.0%; Pred. No. 3,22e-13;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 321 AGGTTACCTCGTCTCGTAAATCTTCTGAAGTAAGG 362
Qy 322 AGGTTACCTCGTCTCGTAAATCTTCTGAAGTAAGG 363
RESULT 3
LOCUS 132407 720 bp DNA PAT 07-JAN-1997
DEFINITION Sequence 2 from patent US 5587458.
ACCESSION I32407
NID 91823198
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 720)
AUTHORS King,C.Richter, Kasprzyk,P.G. and Bird,R.E.
TITLE Anti-erbB-2 antibodies, combinations thereof, and therapeutic and
diagnostic uses thereof
JOURNAL Patent: US 5587458-A 2 24-DEC-1996;
FEATURES
source
1..720
/organism="unknown"
BASE COUNT 184 a 178 c 179 g 179 t
ORIGIN
Query Match 90.5%; Score 38; DB 21; Length 720;
Best Local Similarity 95.2%; Pred. No. 1.36e-10;
Matches 40; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 315 AGGTTACCTCGGATCTGTAATCTTCTGAAGTAAGG 356
Qy 322 AGGTTACCTCGTCTCGTAAATCTTCTGAAGTAAGG 363
RESULT 4
LOCUS MUSALC 846 bp mRNA ROD 11-JUL-1995

DEFINITION Mus musculus (clone pCT.scfv) antibody mRNA, 3' end of cds.
ACCESSION L43543
NID 9896287
KEYWORDS antibody.
SOURCE Mus musculus
ORGANISM Mus musculus (clone: pCT.scfv) cDNA to mRNA.
Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Mus.
REFERENCE 1 (bases 1 to 846)
AUTHORS Paul,S., Sun,M. and Gao,Q.-S.
TITLE Catalysts by natural and hybrid single chain Fv constructs
JOURNAL Unpublished (1995)
FEATURES
source
1..846
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="pCT.scfv"
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/cell_type="hybridoma"
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/db_xref="PID:9896290"
/translation="DVLMTQTPPLTSLVYIGOPASISCKSSQSLHTDCKTYLWLLQR
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translation of the corresponding V_region. Presently
translation qualifiers on V_region features are illegal."
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355..396
/note="putative"
/function="linkers between VL and VH domains"
1..735
/note="putative"
/product="antibody heavy chain"
1..735
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translation of the corresponding V_region. Presently
translation qualifiers on V_region features are illegal."
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736..765
/note="c-myc peptide-1; putative"
/function="facilitates recombinant protein identification"
775..792
/note="poly-histidine; putative"
/function="facilitates recombinant protein purification"
BASE COUNT 213 a 203 c 228 g 202 t
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Query Match 81.0%; Score 34; DB 28; Length 846;
Best Local Similarity 90.5%; Pred. No. 5.00e-08;
Matches 38; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Db 354 AGGTTACCTCGGCTCGGAAATCGTGAAGTAAGG 395

|||||
QY 322 AGGTTCTACCTCTGCTGTCTGTGAATCTTCTGAAGTAAGG 363

RESULT 5
LOCUS MUSALCA 855 bp mRNA ROD 11-JUL-1995
DEFINITION Mus musculus (clone pCT.kvhd1) antibody mRNA, 3' end of cds.
ACCESSION L43544
NID 9896291
KEYWORDS antibody.
SOURCE Mus musculus cDNA to mRNA.
ORGANISM Mus musculus
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 855)
AUTHORS Paul, S., Sun, M. and Gao, Q.-S.
TITLE Catalysis by natural and hybrid single chain Fv constructs
JOURNAL Unpublished (1995)
FEATURES
source Location/Qualifiers
1..855
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<1..354
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<1..855
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745..774
/note="c-myc peptide-1; putative"
/function="facilitates recombinant protein identification"
784..801
/note="poly-histidine; putative"
/function="facilitates recombinant protein purification"
misc_feature
BASE COUNT 231 a 217 c 217 g 190 t
ORIGIN
Query Match 81.0%; Score 34; DB 28; Length 855;
Best Local Similarity 90.5%; Pred. No. 5.00e-08;
Matches 38; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 354 AGGTTCTACCTCCGGCTCTGGGAATCTCTGAAGTAAGG 395
QY 322 AGGTTCTACCTCTGCTGTCTGTGAATCTTCTGAAGTAAGG 363

RESULT 6
LOCUS 132414 47 bp DNA PAT 07-JAN-1997
DEFINITION Sequence 9 from patent US 5587458.
ACCESSION 132414
NID 91823205
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 47)
AUTHORS King, C. Richter, Kasprzyk, P.G. and Bird, R.E.
TITLE Anti-erbB-2 antibodies, combinations thereof, and therapeutic and diagnostic uses thereof
JOURNAL Patent: US 5587458-A 9 24-DEC-1996;
FEATURES
source Location/Qualifiers
1..47
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BASE COUNT 11 a 7 c 16 g 13 t
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Best Local Similarity 100.0%; Pred. No. 3.74e-06;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 CTGCTTCTGTAATCTCTGGAAGTAAGG 31
QY 333 CTGCTTCTGTAATCTCTGGAAGTAAGG 363

RESULT 7
LOCUS 132413 47 bp DNA PAT 07-JAN-1997
DEFINITION Sequence 8 from patent US 5587458.
ACCESSION 132413
NID 91823204
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 47)
AUTHORS King, C. Richter, Kasprzyk, P.G. and Bird, R.E.
TITLE Anti-erbB-2 antibodies, combinations thereof, and therapeutic and diagnostic uses thereof
JOURNAL Patent: US 5587458-A 8 24-DEC-1996;
FEATURES
source Location/Qualifiers
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/organism="unknown"
BASE COUNT 15 a 9 c 10 g 13 t
ORIGIN
Query Match 71.4%; Score 30; DB 21; Length 47;
Best Local Similarity 100.0%; Pred. No. 1.54e-05;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 GAAGATTACCAAGACAGAGTAGAAGCT 30
Cp 351 GAAGATTACCAAGACAGAGTAGAAGCT 322

RESULT 8
LOCUS SYNBET2X 717 bp mRNA SYN 01-MAR-1996
DEFINITION Synthetic single-chain Fv fusion protein (Bet 2/212) mRNA, constructed from variable light and heavy chain regions of rat monoclonal antibody Bet 2, 3' end of cds.
ACCESSION L17036
NID 9310725
KEYWORDS Igm-binding protein; fusion protein; fusion protein Bet 2/212; monoclonal antibody.

SOURCE Artificial gene cDNA to mRNA.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 717)
AUTHORS Lee,T.K., Rollence,M.L., Hallberg,P.L., Oelkelt,M.S., Dodd,S.W., Nagle,J.W. and Filipula,D.R.
TITLE Production of engineered IgM-binding single-chain antibodies in Escherichia coli
JOURNAL J. Ind. Microbiol. 14 (5), 371-376 (1995)
MEDLINE 9538669
FEATURES
source Location/Qualifiers
1..717
/organism="artificial sequence"
/db_xref="taxon:29278"
CDS
1..708
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/product="fusion protein"
/db_xref="PID:g310726"
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misc_feature 1..312
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misc_feature 313..354
/note="linker segment"
misc_feature 355..717
/note="variable heavy chain derived from rat monoclonal antibody Bet 2 (ATCC HB88)"
BASE COUNT 193 a 170 c 186 g 168 t
ORIGIN
Query Match 57.1%; Score 24; DB 31; Length 717;
Best Local Similarity 78.6%; Pred. No. 5.35e-02;
Matches 33; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Db 312 AGGCTTACTTCGCGTAGCGCAATCTCTGAAGCAAGG 353
||| ||||| || || ||||| ||||| ||||| |||||
QY 322 AGGTTCTACTCTGCTTCGTGTAATCTTCTGAAGTAAGG 363
RESULT 9
LOCUS SYN7A41 743 bp DNA SYN 04-MAR-1993
DEFINITION Synthetic single-chain antigen-binding protein gene (7A4-1/212 SCA) constructed from the antigen-binding (Fab) fragment of mouse catalytic monoclonal antibody NPN43C9 and linker DNA, partial cds.
ACCESSION M68968
NID 9207839
KEYWORDS 7A4/212 SCA protein; fusion protein; monoclonal antibody; single-chain antigen-binding protein.
SOURCE Mouse DNA and synthetic DNA.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 743)
AUTHORS Gibbs,R.A., Posner,B.A., Filipula,D.R., Dodd,S.W., Finkelman,M.A., J., Lee,T.K., Wroble,M., Whitlow,M. and Benkovic,S.J.
TITLE Construction and characterization of a single-chain catalytic antibody
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 88, 4001-4004 (1991)
MEDLINE 9121950
FEATURES
source Location/Qualifiers
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/db_xref="taxon:29278"
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misc_feature 1..339
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/note="light-chain variable region of mouse antibody NPN43C9"
misc_feature 340..381
/gene="7A4-1/212"
/note="synthetic linker"
misc_feature 382..735
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/note="heavy-chain variable region of mouse antibody NPN43C9"
BASE COUNT 195 a 176 c 190 g 182 t
ORIGIN
Query Match 57.1%; Score 24; DB 31; Length 743;
Best Local Similarity 78.6%; Pred. No. 5.35e-02;
Matches 33; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
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QY 322 AGGTTCTACTCTGCTTCGTGTAATCTTCTGAAGTAAGG 363
RESULT 10
LOCUS SYND44X 744 bp mRNA SYN 01-MAR-1996
DEFINITION Synthetic single-chain Fv fusion protein (DA4.4/212) mRNA, constructed from variable light and heavy chain regions of mouse monoclonal antibody DA4.4, 3' end of cds.
ACCESSION L17037
NID 9310739
KEYWORDS IgM-binding protein; fusion protein; fusion protein DA4.4/212; monoclonal antibody.
SOURCE Artificial gene cDNA to mRNA.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 744)
AUTHORS Lee,T.K., Rollence,M.L., Hallberg,P.L., Oelkelt,M.S., Dodd,S.W., Nagle,J.W. and Filipula,D.R.
TITLE Production of engineered IgM-binding single-chain antibodies in Escherichia coli
JOURNAL U. Ind. Microbiol. 14 (5), 371-376 (1995)
MEDLINE 9538669
FEATURES
source Location/Qualifiers
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misc_feature 382..744

AUTHORS Vogel,J., Hess,M.R. and Borne,T.
TITLE A comparative analysis of group II introns in chloroplasts of higher plants
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 1636)
AUTHORS Vogel,J.
TITLE Direct Submission
JOURNAL Submitted (05-SEP-1998) Vogel J., Department of Biology (Genetics), Humboldt University, Chausseestraße 117, Berlin D-10115, Germany
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Best Local Similarity 91.78; Pred. No. 8,14e+00;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Cp 348 GATTACAGACAGAGTAGA 325
RESULT 14
LOCUS HPU31780 7368 bp DNA VRL 18-OCT-1995
DEFINITION Human papillomavirus type 22, complete genome.
ACCESSION U31780
NID 91020178
KEYWORDS
SOURCE Human papillomavirus type 22.
ORGANISM Viruses; dsDNA viruses, no RNA stage; Papovaviridae;
Papillomavirus.
REFERENCE 1 (bases 1 to 7368)
AUTHORS Delius,H.
TITLE Sequenced by Hejo Delius, Deutsches Krebsforschungszentrum, Angewandte Tumorstrologie, I.N.F. 506, W-6900 Heidelberg, Germany
JOURNAL Unpublished
REFERENCE 2 (sites)
AUTHORS Kremsdorf,D., Favre,M., Jablonska,S., Obalek,S., Rueda,L.A., Lutzner,M.A., Blanchet-Bardon,C., Van Vooast Vader,P.C. and Orth,G.
TITLE Molecular cloning and characterization of the genomes of nine newly recognized human papillomavirus types associated with epidermodysplasia verruciformis
JOURNAL J. Virol. 52 (3), 1013-1018 (1984)
MEDLINE 85033930
REFERENCE 3 (bases 1 to 7368)
AUTHORS Farmer,A.D.
TITLE Direct Submission

JOURNAL Submitted (18-Jul-1995) Andrew D. Farmer, HTV Sequence Database, Los Alamos National Laboratory, T-10, Mail Stop K710, Los Alamos, NM 87501, USA
COMMENT
HPV22 was originally isolated from macules on the chest of an Italian epidermodysplasia verruciformis (EV) patient [2]. The HPV22 genome, like that of HPVs 9, 15, 17a/b, 23, 37, 38, is smaller than most PV genomes at approximately 7.4 kb. Phylogenetic reconstructions based on DNA sequences of established types indicate that HPV22 is most closely related to HPVs 23 and 38, and then to 15, 17, 37 and 9. Although Kremsdorf et al [2] found substantial cross-hybridization between HPV22 and HPV19, nucleotide sequence comparison fails to support a close relationship between these two types.
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LOCUS	AE001306	13316 bp	DNA
DEFINITION	Chlamydia trachomatis section 33 of 87 of the complete genome.		
ACCESSION	AE001306	AE001273	
NID	9328748		
KEYWORDS	Chlamydia trachomatis.		
SOURCE	Chlamydia trachomatis		
ORGANISM	Eubacteria; Chlamydiales; Chlamydiaceae; Chlamydia.		
REFERENCE	1	(bases 1 to 13316)	
AUTHORS	Stephens, R.S., Kalman, S., Lammel, C.J., Fan, J., Marathe, R., Aravind, L., Mitchell, W.P., Olinger, L., Tatusov, R.L., Zhao, Q., Koonin, E.V. and Davis, R.W.		
TITLE	Genome Sequence of an Obligate Intracellular Pathogen of Humans: Chlamydia trachomatis		
JOURNAL	Science (1998) In press		
REFERENCE	2 (bases 1 to 13316)		
AUTHORS	Stephens, R.S., Kalman, S., Lammel, C.J., Fan, J., Marathe, R., Aravind, L., Mitchell, W.P., Olinger, L., Tatusov, R.L., Zhao, Q., Koonin, E.V. and Davis, R.W.		
TITLE	Direct Submission		
JOURNAL	Submitted (20-MAY-1998) Program in Infectious Diseases, University of California, 235 Warren Hall, Berkeley, CA 94720-7360, USA		
FEATURES	Location/Qualifiers		
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Best Local Similarity 95.5%; Pred. No. 8.14e+00;
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QY 331 CTCGTGTTCTGTAATCTTCT 352
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Search completed: Sat Jan 9 17:12:39 1999
Job time : 107 secs.

WIRESENSE (TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
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Msrch_n n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Sat Jan 9 17:20:30 1999; MasPar time 20.09 Seconds
Tabular output not generated. 284,402 Million cell updates/sec

Title: >US-08-704-178-1
Description: (322-363) from US08704178.seq (4 of 4)
Perfect Score: 42
N.A. Sequence: 322 AGGTTCTACCTCTGGTCTGTAATCTTCTGAGAGTAAGG 363
Comp: TCCAGATGAGAGACCAAGCATTATAGAGACTTCATTCC

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 188442 segs, 68026449 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: n-genseq32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
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39:part39 40:part40

Statistics: Mean 5.992; Variance 4.139; scale 1.448

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	42	100.0	711 18	Anti-erbB2 scFv cDNA.	4,08e-12
3	42	100.0	711 29	Single-chain anti-erb	4,08e-12
4	42	100.0	761 7	Sequence encoding a 4	4,08e-12
5	42	100.0	803 3	Om212 single chain an	4,08e-12
6	38	90.5	720 29	Single-chain anti-erb	6,29e-10
7	38	90.5	720 9	Sequence encoding the	6,29e-10
8	38	90.5	731 7	Sequence encoding a m	6,29e-10
9	38	90.5	770 7	Sequence encoding a m	6,29e-10
10	32	76.2	91 9	Oligonucleotide probe	1,03e-06
11	28	66.7	744 7	Sequence encoding a m	1,24e-04
12	25	59.5	91 9	Oligonucleotide probe	4,10e-03
13	24	57.1	797 22	CC49/212 SCA PLAP DNA	1,29e-02

14	24	57.1	803 22	T29059	PIAP CC49/212 SCA DNA	1,29e-02
15	24	57.1	1460 7	043291	Sequence encoding div	1,29e-02
16	23	54.8	738 7	043293	Sequence encoding sin	4,00e-02
17	23	54.8	738 11	066841	CC49 VL / 217 / 4-4-2	4,00e-02
18	21	50.0	39 7	051787	Mixed oligonucleotide	3,70e-01
19	21	50.0	47 35	T86394	Sp6 anti-TNP antibody	3,70e-01
20	21	50.0	66 8	049187	scFvR construction pr	3,70e-01
21	20	47.6	36 2	011195	Ballast construction c	1,10e+00
22	20	47.6	50 13	080512	Primer used in immuno	1,10e+00
23	20	47.6	725 11	066840	4-4-20 VL/ 217 / CC49	1,10e+00
24	20	47.6	725 7	043292	Sequence encoding sin	1,10e+00
25	20	47.6	5600 3	022963	Sequence encoding sin	1,10e+00
26	20	47.6	5600 11	062653	PHCV-31 plasmid expre	1,10e+00
27	20	47.6	5600 6	038265	HCV CRK-33-BCD fusion	1,10e+00
28	20	47.6	5600 6	038251	HCV CRK-33-BCD fusion	1,10e+00
29	20	47.6	5600 3	021678	PHCV-31 - recombinant	1,10e+00
30	20	47.6	5600 6	038236	HCV CRK-33-BCD expres	1,10e+00
31	19	45.2	5362 39	T97296	Mouse additional sex	3,21e+00
32	19	45.2	5362 39	T97294	Mouse additional sex	3,21e+00
33	19	45.2	9202 2	N70608	Visna sheep lentiviru	3,21e+00
34	18	42.9	33 7	046603	Mixed oligonucleotide	9,18e+00
35	18	42.9	1144 10	044800	Encodes single-strand	9,18e+00
36	18	42.9	1144 38	T99264	Human PUR-alpha gene.	9,18e+00
37	18	42.9	2956 37	T99140	Full length cytochrom	9,18e+00
38	18	42.9	3279 9	050946	Sequence encoding pro	9,18e+00
39	18	42.9	3279 9	051556	Sequence encoding pro	9,18e+00
40	18	42.9	3388 34	T84543	Human steroid recepto	9,18e+00
41	18	42.9	3399 20	T05868	Chicken leucocytozoan	9,18e+00
42	18	42.9	134525 1	004525	Total base sequence o	9,18e+00
43	17	40.5	563 1	N90964	Sequence in a recombi	2,57e+01
44	17	40.5	668 1	006496	IFN-alpha 61 gene and	2,57e+01
45	17	40.5	3537 1	006831	Sequence encoding B.c	2,57e+01

ALIGNMENTS

RESULT 1
ID Q55180 standard; cDNA; 711 BP.
AC Q55180;
DT 21-JUL-1994 (first entry)
DE Sequence encoding the single chain anti-erbB2 antibody, Ab no.23.
KW Single chain anti-erbB2 antibody; cancer therapy; prevention;
KM monoclonal antibody; ss.
OS Synthetic.
FH Key Location/Qualifiers
FT cds 1..171
FT 1..171
FT /*tag= a
PN MO9400136-A.
PD 06-JAN-1994.
PE 21-OCT-1992; U08545.
PR 30-JUN-1992; US-906555.
PA (MOLE-) MOLECULAR ONCOLOGY INC.
PI Kasprzyk PG, King CR;
DR WPI; 94-025878/03.
DR P-PSDB; R45442.
PT Treatment of malignancies over-expressing ERB-12 - using at least
PT 2 monoclonal antibodies which recognise different epitopes on
PT gp185
PS Example: Fig 7; 37pp: English.
CC The source of human erbB-2 protein for the prodn. of antibodies no.
CC 23 and 21 (Q55180/R45442; Q55181/R45443) is a NIH/3T3 cell
CC engineered to express the human erbB-2 protein on its surface (N/
CC erbB-2). Abs no. 21 and 23 are directed against the extracellular
CC domain of gp185 erbB-2. Nude mice manipulated to produce rapidly
CC growing tumours were used in a trial of the efficacy of the Abs. In
CC animals given a combination of the 2 Abs, tumours completely
CC regressed after 11 days.
SQ Sequence 711 BP; 175 A; 183 C; 187 G; 165 T;

Query Match 100.0%; Score 42; DB 9; Length 711;
Best Local Similarity 100.0%; Pred. No. 4,08e-12;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 321 aggtctaccctctgtctgtaaatctctgaagtaag 362
|||||
OY 322 AGGTTCTACTCTGTGTTCTGTAATCTTCTGAAGTAAGG 363

RESULT 2
ID T17728 standard; cDNA: 711 BP.
AC T17728: (first entry)
DE 21-MAY-1996 (first entry)
KW Oncoprotein; erbB2; cell proliferation; tumour; cancer;
intracellular antibody homologue; single chain antibody; scfv;
gene therapy; ds.
OS Synthetic.
PN WO9607321-A1.
PD 14-MAR-1996.
PF 23-AUG-1995: US-010740.
PR 06-SEP-1994: US-301339.
PR 06-JUN-1995: US-468252.
PA (UNABR-) UAB RES. FOUND.
PI Curial DT, Deshane J.
DR WPI: 96-171307/17.
P-PSDB: R94020.
PT Inhibition of proliferation or survival of, esp. malignant erbB2,
PT cells - by introducing nucleic acid mol. encoding antibody homologue
PT which is expressed and binds, pref. erbB2, protein intracellularly
PS Claim 42: Page 29-30: 48pp; English.
CC A nucleic acid comprises a first sequence encoding a signal peptide
CC (R94019) linked to a second sequence (T17728) encoding a single
CC chain FV fragment (R94020) that binds a human erbB2 oncoprotein.
CC The anti-erbB2 scfv portion is obtained by PCR using e23scfv
CC plasmid as template. The signal peptide directs the scfv to the
CC endoplasmic reticulum. The nucleic acid is incorporated into a
CC plasmid or viral vector to facilitate expression of the scfv antibody
CC homologue within e.g. an epithelial carcinoma cell. Intracellular
CC expression of the homologue inhibits surface expression of erbB2 and
CC thereby inhibits cell proliferation and cell survival and decreases
CC tumorigenicity.
SQ Sequence 711 BP; 175 A; 183 C; 189 G; 164 T;

Query Match 100.0%; Score 42; DB 18; Length 711;
Best Local Similarity 100.0%; Pred. No. 4, 08e-12;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 321 aggtctaccctctgtctgtaaatctctgaagtaag 362
|||||
OY 322 AGGTTCTACTCTGTGTTCTGTAATCTTCTGAAGTAAGG 363

RESULT 3
ID T65006 standard; cDNA: 711 BP.
AC T65006:
DE 05-JUN-1997 (first entry)
DE Single-chain anti-erbB2 antibody e23(FV) cDNA.
KW Single chain antibody; variable region; light chain; heavy chain;
breast cancer; ovarian cancer; non-small cell lung carcinoma;
immunodiagnostics; treatment; cytotoxic agent; erbB-2; ds.
OS Mus musculus.
OS Synthetic.
FH Key Location/Qualifiers
FT mat_peptide 1..711
FT /*tag- a
FT /*product- e23(FV)

US5587458-A.
PD 24-DEC-1996.
PF 07-OCT-1991: 772270.
PR 07-OCT-1991: US-772270.
PR 30-JUN-1992: US-906555.
PR 14-MAY-1993: US-061092.
PA (ARON-) ARONEX PHARM INC.
PI Bird RE, Kasprzyk PG, King CR;
DR WPI: 97-064831/06.
P-PSDB: W15185.

PT Single chain antibodies specific for erbB-2 protein, gp185 - with
PT labels or cytotoxin, useful for detection and treatment of tumour
PT cells expressing this protein
PS Example 8; Columns 25-28; 28pp; English.
CC The present cDNA sequence codes for a claimed single-chain antibody e23,
CC designated e23(FV), which binds to erbB-2. Monoclonal antibody e23,
CC was generated by immunising mice with N/erbB-2 cells overexpressing
CC the gp185 protein, removing spleen cells and producing hybridomas
CC by standard techniques. Messenger RNA coding for the anti-erbB-2
CC monoclonal antibody was isolated and converted to cDNA. Regions
CC coding for the heavy- and light- chain variable regions were then
CC amplified by PCR and joined via a sequence encoding a peptide
CC linker. The resulting single-chain antibody is useful for in vitro
CC diagnosis of tumour cells which overexpress the erbB-2 gp185
CC marker, e.g. breast, ovarian and non-small cell lung carcinomas,
CC and, when coupled to a cytotoxic agent, to treat such tumours.
SQ Sequence 711 BP; 175 A; 182 C; 189 G; 164 T;

Query Match 100.0%; Score 42; DB 29; Length 711;
Best Local Similarity 100.0%; Pred. No. 4, 08e-12;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 321 aggtctaccctctgtctgtaaatctctgaagtaag 362
|||||
OY 322 AGGTTCTACTCTGTGTTCTGTAATCTTCTGAAGTAAGG 363

RESULT 4
ID Q43289 standard; DNA: 761 BP.
AC Q43289:
DE 27-SEP-1993 (first entry)
DE Sequence encoding a 4'-4-20/212 single-chain antigen-binding
DE protein with a single cysteine hinge.
KW Antibody; multivalent; variable region; heavy chain; light chain;
linker; ss.
OS Synthetic.
FH Key Location/Qualifiers
FT cds 1..761
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FT /*tag- zx
FT /*tag- zy
FT /*tag- zz

CC from a cysteine to a serine. The hinge regions were added by
CC introduction of a BstE II restriction site in the 3'-terminus
CC of the gene encoding the 4-4-20/212 single-chain antigen-binding
CC protein.
SQ Sequence 761 BP; 212 A; 162 C; 187 G; 200 T;
Query Match 100.0%; Score 42; DB 7; Length 761;
Best Local Similarity 100.0%; Pred. No. 4,08e-12;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 336 aggtctaccctcgtctcgtgaatactctcgaagtaag 377
|||||
Oy 322 AGCTTCTACCTCTGCTTGTGTAATCTTCGAGTAAG 363
RESULT 5
ID 014831 standard; DNA: 803 BP.
AC 014831.
DT 17-FEB-1992 (first entry)
DE Qm212 single chain antigen binding protein with metal binding site.
KW Antigen binding; metal cations; ss.
FH Key Location/Qualifiers
FT cds 1..272
FT /tag= a
FT MO9116912-A.
PD 14-NOV-1991.
PF 07-MAY-1991; U03149.
PR 08-MAY-1990; US-521258.
PR 18-JUN-1990; US-539980.
PA (SCRI-) SCRIPPS CLINIC & RE.
PI Lerner RA, Roberts VN, Getroff ED, Tainer JA, Benkovic SJ;
DR WPI: 91-353518/48.
DR P-PSDB: R15055.
PT New metal binding proteins - comprising variable domain of
PT immunoglobulin and 3 contact aminoacid residues as metal binding
PT site
PS Disclosure: Fig 1; 73pp; English
CC The sequence encodes Qm212, a single chain antigen binding protein
CC having a metal binding site which is derived from the 4-4-20/212
CC protein (Bird et al., Science, 242:423-426 (1988)). Qm212 differs
CC from 4-4-20/212 by amino acid substitutions at residue positions
CC 60, 62, 115 and 117 to provide for contact amino acid residues,
CC where three of these contact residues form a metal binding site.
CC The organism from which the gene originated is not given in the
CC specification. The protein may be used to selectively partition
CC and/or remove metal cations from fluids. Preselcted antigens can
CC be used to remove metal-protein complexes from a liquid phase or as
CC indicators of metal complex formation. The metal-protein complexes
CC can also be used to promote a predetermined chemical reaction, e.g.
CC hydrolysis of a peptide bond.
CC Sequence 803 BP; 224 A; 175 C; 197 G; 207 T;
SQ
Query Match 100.0%; Score 42; DB 3; Length 803;
Best Local Similarity 100.0%; Pred. No. 4,08e-12;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 399 aggtctaccctcgtctcgtgaatactctcgaagtaag 440
|||||
Oy 322 AGCTTCTACCTCTGCTTGTGTAATCTTCGAGTAAG 363
RESULT 6
ID T65007 standard; cDNA: 720 BP.
AC T65007.
DT 05-JUN-1997 (first entry)
DE Single-chain anti-erbB2 antibody e21(Fv) cDNA.
KW Single chain antibody; variable region; light chain; heavy chain;
KW breast cancer; ovarian cancer; non-small cell lung carcinoma;
KW immunodiagnosis; treatment; cytotoxic agent; erbB-2; ds.
OS Mus musculus.
OS Synthetic.
FH Key Location/Qualifiers
FT mat_peptide 1..720

FT /tag= a
FT /product= e21(Fv)
FN US5587458-A.
PD 24-DEC-1996.
PF 07-OCT-1991; 772270.
PR 07-OCT-1991; US-772270.
PR 30-JUN-1992; US-906555.
PR 14-MAY-1993; US-061092.
PA (ARON-) ARONEX PHARM INC.
PI Bird RE, Kasprzyk PG, King CR;
DR WPI: 97-064831/06.
DR P-PSDB: W15186.
PT Single chain antibodies specific for erbB-2 protein, gp185 - with
PT labels or cytotoxin, useful for detection and treatment of tumour
PT cells expressing this protein
PS Example 9; Columns 27-30; 28pp; English.
CC The present cDNA sequence codes for a claimed single-chain antibody,
CC designated e21(Fv), which binds to erbB-2. Monoclonal antibody e21
CC was generated by immunising mice with N/erbB-2 cells overexpressing
CC the gp185 protein, removing spleen cells and producing hybridomas
CC by standard techniques. Messenger RNA coding for the anti-erbB-2
CC monoclonal antibody was isolated and converted to cDNA. Regions
CC coding for the heavy- and light- chain variable regions were then
CC amplified by PCR and joined via a sequence encoding a peptide
CC linker. The resulting single-chain antibody is useful for in vitro
CC diagnosis of tumour cells which overexpress the erbB-2 gp185
CC marker, e.g. breast, ovarian and non-small cell lung carcinomas,
CC and, when coupled to a cytotoxic agent, to treat such tumours.
SQ Sequence 720 BP; 184 A; 178 C; 179 G; 179 T;
Query Match 90.5%; Score 38; DB 29; Length 720;
Best Local Similarity 95.2%; Pred. No. 6,29e-10;
Matches 40; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 315 aggtctaccctcgtcgtgaatactctcgaagtaag 356
|||||
Oy 322 AGCTTCTACCTCTGCTTGTGTAATCTTCGAGTAAG 363
RESULT 7
ID 055181 standard; cDNA: 720 BP.
AC 055181.
DT 21-JUL-1994 (first entry)
DE Sequence encoding the single chain anti-erbB2 antibody, Ab no. 21.
KW Single chain anti-erbB1 antibody; cancer therapy; prevention;
KW monoclonal antibody; ss.
OS Synthetic.
FH Key Location/Qualifiers
FT cds 1..171
FT /tag= a
FT MO9400136-A.
PD 06-JAN-1994.
PF 21-OCT-1992; U08545.
PR 30-JUN-1992; US-906555.
PA (MOLE-) MOLECULAR ONCOLOGY INC.
PI Kasprzyk PG, King CR;
DR WPI: 94-025878/03.
DR P-PSDB: R45443.
PT Treatment of malignancies over-expressing ERB-12 - using at least
PT 2 monoclonal antibodies which recognise different epitopes on
PT gp185
PS Example; Fig 8; 37pp; English.
CC The source of human erbB-2 protein for the prodn. of antibodies no.
CC 23 and 21 (055180/R45442; 055181/R45443) is a NIH/3T3 cell
CC engineered to express the human erbB-2 protein on its surface (N/
CC erbB-2). Abs no. 21 and 23 are directed against the extracellular
CC domain of gp185 erbB-2. Nude mice manipulated to produce rapidly
CC growing tumours were used in a trial of the efficacy of the Abs. In
CC animals given a combination of the 2 Abs, tumours completely
CC regressed after 11 days.
SQ Sequence 720 BP; 184 A; 178 C; 179 G; 179 T;
Query Match 90.5%; Score 38; DB 9; Length 720;

SQ Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
 Query Match 76.2%; Score 32; DB 9; Length 91;
 Best Local Similarity 0.0%; Pred. No. 1.03e-06;
 Matches 0; Conservative 35; Mismatches 3; Indels 0; Gaps 0;
 Db 20 hvvshhsvhvhhvhhvhhvhhvhhvhhvhhv 57
 CP 359 TACCTCAGAGATTTCACGACCAGAGTAGAAGCT 322
 RESULT 11
 ID 043288 standard; DNA; 744 BP.
 AC 043288;
 DT 27-SEP-1993 (first entry)
 DE Sequence encoding a multivalent antigen-binding single-chain protein
 comprising the CC49 VL region connected through the 212 linker
 DE polypeptide to the 4-4-20 VH region.
 KW Antibody; multivalent; variable region; heavy chain; light chain;
 linker; ss.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT cds 1..744
 FT /tag- a
 FT cds 1..339
 FT /tag- b
 FT /product= CC49 VL
 FT cds 340..381
 FT /tag- c
 FT /product= 212 linker
 FT cds 382..732
 FT /tag- d
 FT /product= 4-4-20 VH
 FT MO9311161-A.
 PN 10-JUN-1993.
 PD 20-NOV-1992; U09965.
 PR 25-NOV-1991; US-796936.
 PA (ENZO-) ENZON INC.
 PI Bird RE, Filpula D, Hardman K, Rolence M, Whitlow MD,
 PI Wood JF;
 DR WPI: 93-196999/24.
 DR P-PSDB: R37646.
 PT New multivalent antigen-binding protein e.g. contg. CC49 Mab
 PT regions - useful in diagnosis, for destroying blood clots and
 PT targeting cytotoxic agents or enzymes to tumour cells
 PS Example 1; Fig 10B; 118bp; English.
 CC "4-4-20 VH" means the variable region of the heavy chain of the
 CC 4-4-20 mouse monoclonal antibody (Bird, R.E. et al., Science 242:423
 CC (1988)). The number "212" refers to a specific 14-residue
 CC polypeptide linker that links the 4-4-20 VH and the CC49 VL. See
 CC Bedzyk, W.D. et al., J. Biol. Chem. 265:18615-18620 (1990). "CC49 VL"
 CC is the variable region of the light chain of the CC49 antibody,
 CC which binds to the TAG-72 antigen.
 SQ Sequence 744 BP; 199 A; 164 C; 185 G; 196 T;
 Query Match 66.7%; Score 28; DB 7; Length 744;
 Best Local Similarity 83.3%; Pred. No. 1.24e-04;
 Matches 35; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 Db 339 aggcctactccgtagcggaacatctctgaaggtaaag 380
 OY 322 AGGTTTACTCTGTTCTGTGTAATCTTGAAGTAAGG 363
 RESULT 12
 ID 051746 standard; cDNA; 91 BP.
 AC 051746;
 DT 31-MAY-1994 (first entry)
 DE Oligonucleotide probe MK14-A
 KW Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
 OS Synthetic.
 PN EP-571911-A.

PD 01-DEC-1993.
 PF 24-MAY-1993; 108325.
 PR 26-MAY-1992; US-869651.
 PA (BECT) BECTON DICKINSON CO.
 PI Shank DD, Spears PA;
 DR WPI: 93-378844/48.
 PT New oligo:nucleotide probes specific for Mycobacteria - used for
 PT detection and amplification of Mycobacteria nucleic acid in
 PT samples
 PS Claim 3; Page 14; 23pp; English.
 CC Oligonucleotide probe MK14-A consists of nucleotides 5-95 of MK14
 CC (051735). It hybridized to all spp. of mycobacteria tested, but
 CC cross reacted to a few non-mycobacterial spp. The probe may
 CC be useful as an initial screen for mycobacterial infection.
 CC See also 051735-45 and 051747-59.
 SQ Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
 Query Match 59.5%; Score 25; DB 9; Length 91;
 Best Local Similarity 0.08; Pred. No. 4.10e-03;
 Matches 0; Conservative 31; Mismatches 6; Indels 0; Gaps 0;
 Db 13 vhsyvvhvshsvhhvhhvsvvvvhhvhhv 49
 OY 327 CTACCTCTGTTCTGTGTAATCTTGAAGTAAGG 363
 RESULT 13
 ID T29058 standard; DNA; 797 BP.
 AC T29058;
 DT 03-OCT-1996 (first entry)
 DE CC49/212 SCA PLAP DNA construct.
 KW Single-chain antigen-binding fusion protein; SCA; immunoeffector;
 KW cytosolic; phospholipase A activating protein; PLAP; cancer;
 KW therapy; monoclonal antibody; CC49; ds.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT cds 1..789
 FT /tag- a
 FT /product= CC49 VL-212 linker-VH-PLAP fusion
 FT MO9611955-A1.
 PN 25-APR-1996.
 PD 13-OCT-1995; U12840.
 PR 13-OCT-1994; US-323445.
 PA (ENZO-) ENZON INC.
 PI Filpula D, Short R, Whitlow M;
 DR WPI: 96-221949/22.
 DR P-PSDB: R97380.
 PT New antigen binding proteins contg. immunoeffector or cytolytic
 PT peptide - attached to variable regions of antibody light or heavy
 PT chain, useful in diagnosis and in destroying cancer cells
 PS Example 1; Fig 4A-B; 72pp; English.
 CC A novel DNA construct (T29058) codes for a single-chain antigen-
 CC binding fusion protein (R97380) comprising the light chain variable-
 CC region (VL) of monoclonal antibody CC49 linked to the CC49 VH
 CC region via a spacer peptide (R97379). With a C-terminal
 CC phospholipase A activating protein (PLAP) immunoeffector peptide
 CC (R97368). It was obtd. by ligating a synthetic PLAP fragment to an
 CC existing CC49/212 gene, and can be used to produce the fusion
 CC protein in transformed host cells. The fusion protein combines
 CC the tumour antigen-binding capability of CC49 with the
 CC immunoeffector function of PLAP.
 SQ Sequence 797 BP; 196 A; 203 C; 195 G; 203 T;
 Query Match 57.1%; Score 24; DB 22; Length 797;
 Best Local Similarity 78.6%; Pred. No. 1.29e-02;
 Matches 33; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 Db 339 aggcctactccgtagcggaacatctctgaaggtaaag 380
 OY 322 AGGTTTACTCTGTTCTGTGTAATCTTGAAGTAAGG 363
 RESULT 14

ID T29059 standard: DNA: 803 BP.
AC T29059;
DE 03-OCT-1996 (first entry)
DT PLAP CC49/212 SCA DNA construct.
KW Single chain antigen-binding fusion protein; SCA; immunoeffector;
KW cytostatic; phospholipase A activating protein; PLAP; cancer;
OS therapy: monoclonal antibody; CC49; ds.
FH key
FT Location/Qualifiers
FT 1..795
FT /tag= a
FT /product= PLAP CC49 VL-212 linker-VH fusion
PN W09611955-A1.
PD 25-APR-1996
PF 13-OCT-1995; U12840.
PR 13-OCT-1994; US-323445.
PI (ENZO-) ENZON INC.
PI Filpula D, Shorr R, Whitlow M;
PI WPI: 96-221949/22.
DR P-PSDB: R97381.
PT New antigen binding proteins contg. immunoeffector or cytolytic
PT peptide - attached to variable regions of antibody light or heavy
PT chain, useful in diagnosis and in destroying cancer cells
PS Disclosure: Page 39-40; 72pp; English.
CC A novel DNA construct (T29059) codes for a single-chain antigen
CC binding fusion protein (R97381) comprising the light chain variable
CC region (VL) of monoclonal antibody CC49 linked to the CC49 VH
CC region via a spacer peptide (R97379) and with an N-terminal
CC phospholipase A activating protein (PLAP) immunoeffector peptide
CC (R97368). It can be used to produce the fusion protein in
CC transformed host cells. The fusion protein combines the tumour
CC antigen-binding capability of CC49 with the immunoeffector function
CC of PLAP.
SQ Sequence 803 BP; 198 A; 205 C; 196 G; 204 T;

Query Match 57.1%; Score 24; DB 22; Length 803;
Best Local Similarity 78.6%; Pred. No. 1.29e-02;
Matches 33; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 408 aggcctactctccgtagcgcaatcctctgaagcaag 449
||| ||||| || ||| ||| ||||| |||||
QY 322 AGGTTCTACTCTGCTGTCTGTGAATCTCTGAAGTAAG 363

RESULT 15
ID Q43291 standard: DNA: 1460 BP.
AC Q43291;
DE 27-SEP-1993 (first entry)
DT Sequence encoding divalent CC49/212 single-chain antigen-binding
DE protein.
KW Antibody; multivalent; variable region; heavy chain; light chain;
KW linker; ss.
OS Synthetic.
FH key
FT Location/Qualifiers
FT 1..1458
FT /tag= a
FT /tag= b
FT /tag= b
FT /product= CC49 VL
FT 340..374
FT /tag= C
FT /product= 212 linker
FT 375..426
FT /tag= d
FT /product= CC49 VH
FT 427..1065
FT /tag= e
FT /product= CC49 VL
FT 1066..1107
FT /tag= f
FT /product= 212 linker
FT 1108..1449
FT /tag= g

FT W09311161-A.
PN 10-JUN-1993.
PD 20-NOV-1992; U09965.
PF 25-NOV-1991; US-796936.
PR (ENZO-) ENZON INC.
PI Bird RE, Filpula D, Hardman K, Rollence M, Whitlow MD,
PI Wood JR.
PI WPI: 93-196999/24.
DR P-PSDB: R37649.
PT New multivalent antigen-binding protein e.g. contg. CC49 Mab
PT regions - useful in diagnosis, for destroying blood clots and
PT targeting cytotoxic agents or enzymes to tumour cells
PS Example: Fig 16A; 118pp; English.
CC The number 212 refers to a 14-residue linker. CC49 is the CC49
CC antibody.
SQ Sequence 1460 BP; 363 A; 364 C; 365 G; 368 T;

Query Match 57.1%; Score 24; DB 7; Length 1460;
Best Local Similarity 78.6%; Pred. No. 1.29e-02;
Matches 33; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 339 aggcctactctccgtagcgcaatcctctgaagcaag 380
||| ||||| || ||| ||| ||||| |||||
QY 322 AGGTTCTACTCTGCTGTCTGTGAATCTCTGAAGTAAG 363

Search completed: Sat Jan 9 17:20:55 1999
Job time : 25 secs.

Db 206 TTCTTCCTCTGCTTCGACATCTTC 232
 1111 1111111111 111111
 Qy 325 TTCTACCTCTGCTTCGTAAATCTTC 351

RESULT 2
 LOCUS AA754459 252 bp mRNA EST 20-JAN-1998
 DEFINITION 975N1787 Rice Immature Seed Lambda ZAPIT CDNA Library Oryza sativa
 CDNA clone 975N1787, mRNA sequence.
 ACCESSION AA754459
 NID 92801165
 KEYWORDS EST.
 SOURCE rice.
 ORGANISM Oryza sativa
 Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;
 Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;
 Poales; Poaceae; Oryza.
 1 (bases 1 to 252)
 Nahm,B.H., Kim,W.Y., Cheong,J.U., Kim,S.I., Nahm,T.R., Moon,E.P.,
 Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y.,
 Lee,M.C., and Eun,M.Y.
 Large-scale Sequencing Analysis of ESTs from Rice Immature Seed
 Unpublished (1998)

TITLE
 JOURNAL
 COMMENT

REFERENCE
 AUTHORS
 CONTACT: Eun M.Y.
 Department of Cytogenetics
 National Inst. of Agri. Sci. and Tech, RDA
 Suwon, Kyunggi-do, Korea
 Tel: 82 331 290 0301
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 Email: myeun@snu20.asi.re.kr
 Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
 University, Yongin, Korea. 449-728 binahm@bioserver.myongji.ac.kr
 Seq primer: M13 Reverse primer.
 Location/Qualifiers
 1..252
 /organism="Oryza sativa"
 /cultivar="Milyang23"
 /note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
 XhoI; Directional CDNA library inserted into lambda ZAPIT
 vector at 5' end with EcoRI and 3' end with Xho I site."
 /db_xref="taxon:4530"
 /clone="975N1787"
 /clone_lib="Rice Immature Seed Lambda ZAPIT CDNA Library"
 /tissue_type="Immature Seed"
 /dev_stage="5 days after pollination"
 /lab_host="E. coli SOLR"
 BASE COUNT 5 a 21 c 12 g 35 t 179 others
 ORIGIN

Query Match 47.6%; Score 20; DB 12; Length 252;
 Best Local Similarity 6.2%; Pred. No. 6.51e-05;
 Matches 2; Conservative 22; Mismatches 8; Indels 0; Gaps 0;
 Db 99 RBVTRAHYDTCNBRYNNNDYHMHMBMYB 130
 Qy 322 AGGTTCTACCTCTGCTTCGTAAATCTTCG 353

RESULT 3
 LOCUS AA708932 477 bp mRNA EST 24-DEC-1997
 DEFINITION Z164d01.s1 Soares pregnant uterus NBHPU Homo sapiens CDNA clone
 506889.3', mRNA sequence.
 ACCESSION AA708932
 NID 92718850
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
 Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 477)
 Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,

TITLE
 JOURNAL
 COMMENT

REFERENCE
 AUTHORS
 CONTACT: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lln.gov) for further information.
 Seq primer: -40m13 fwd, 5' from Amersham.
 Location/Qualifiers
 1..477
 /organism="Homo sapiens"
 /note="Organ: uterus; Vector: pT73-Pac; Site_1: Not I;
 Site_2: Eco RI; 1st strand CDNA was primed with a Not I -
 01190(dT) primer [5'
 AACTGAGAGATTCGCGCGCCCTTTTCTTTTCTTTT 3']
 double-stranded CDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT73 vector. Library
 went through one round of normalization. Library
 constructed by M. Fatima Bonaldo."
 /db_xref="GDB:3812708"
 /clone="506689"
 /clone_lib="Soares pregnant uterus NBHPU"
 /sex="female"
 /dev_stage="adult"
 /lab_host="DH10B"
 BASE COUNT 144 a 88 c 96 g 149 t
 ORIGIN

Query Match 47.6%; Score 20; DB 11; Length 477;
 Best Local Similarity 88.5%; Pred. No. 6.51e-05;
 Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Db 353 TCTACCTCTGCTTCGTAAATCTTC 378
 Qy 326 TCTACCTCTGCTTCGTAAATCTTC 351

RESULT 4
 LOCUS H41340 217 bp mRNA EST 31-JUL-1995
 DEFINITION Y091f01.r1 Homo sapiens CDNA clone 175801.5', similar to SP:A45036
 A45036 PUR ALPHA-SINGLE-STRANDED-DNA-BINDING PROTEIN - :.
 H41340
 ACCESSION H41340
 NID 9917392
 KEYWORDS EST.
 SOURCE Homo sapiens clone-175801 library-Soares adult brain N2B5HB55Y
 vector-pT73P (Pharmacia) with a modified polylinker host-DH10B
 (ampicillin resistant) primer-M13RP1 Rsite1-Not I Rsite2-Eco RI
 55-year old male. 1st strand CDNA was primed with a Not I -
 01190(dT) primer [5'
 TGTTCACCACTGAGATCGAGCGCGCCCTTTTCTTTTCTTTT 3']
 double-stranded CDNA was size selected, ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I and Eco
 RI sites of a modified pT73 vector (Pharmacia). Library went
 through one round of normalization to a Cot = 53. Library
 constructed by Bento Soares and M. Fatima Bonaldo. The adult brain
 RNA was provided by Dr. Donald H. Gilden. Tissue was acquired 17-18
 hours after death which in consequence of a ruptured
 aortic aneurysm. RNA was prepared from a pool of tissues
 representing the following areas of the brain: frontal, parietal,
 temporal and occipital cortex from the left and right hemispheres,
 subcortical white matter, basal ganglia, thalamus, cerebellum,
 midbrain, pons and medulla.
 Homo sapiens
 Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;

/tissue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"

BASE COUNT 7 a 16 c 21 g 34 t 169 others
ORIGIN

Query Match 45.2%; Score 19; DB 12; Length 247;
Best Local Similarity 11.4%; Pred. No. 1.05e-03;
Matches 4; Conservative 22; Mismatches 9; Indels 0; Gaps 0;

Db 113 SVYVWBTAYCDYBHYBRANHYDTRCTNDRGYC 147
Cp 357 CCTTCGAGAGATTACACAGACAGGTGAAC 323

RESULT 7 HUM184D07B 259 bp mRNA EST 21-MAY-1996
LOCUS Human fetal brain cDNA 5'-end GEN-184D07, mRNA sequence.
DEFINITION
ACCESSION D61368
NID 9963007
KEYWORDS EST: EST(expressed sequence tag); Human fetal brain; similar to none(May 29,1995).
SOURCE Homo sapiens cDNA to mRNA, clone_1lb:Clontech human fetal brain polyA+ mRNA (#6535).
ORGANISM Homo sapiens
Eukaryota; Eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homindaee; Homo.
REFERENCE 1 (bases 1 to 259)
AUTHORS Fujiwara,T., Hirano,H., Katagiri,T., Kawai,A., Kuga,Y., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y., Shinomiya,H., Takeichi,A., Takeda,S., Watanabe,T., Takahashi,E., Hirai,Y., Maeawa,H., Shin,S. and Nakamura,Y.
TITLE Unpublished(1995)
JOURNAL Unpublished(1995)
REFERENCE 2 (bases 1 to 259)
AUTHORS Fujiwara,T.
TITLE Direct Submission
JOURNAL Submitted (30-MAY-1995) to the DDBJ/EMBL/GenBank databases. Tsutomu Fujiwara, Otsuka GEN Research Institute,Otsuka Pharmaceutical Co.,Ltd; 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01, Japan (Tel:0886-65-2888, Fax:0886-37-1035)
COMMENT Submitted (30-May-1995) to DDBJ by:
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Japan
Phone : 0886-65-2888
Fax : 0886-37-1035.

FEATURES
source 1..259
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1lb="Clontech human fetal brain polyA+ mRNA (#6535)"

BASE COUNT 73 a 35 c 45 g 80 t 26 others
ORIGIN

Query Match 45.2%; Score 19; DB 7; Length 259;
Best Local Similarity 59.5%; Pred. No. 1.05e-03;
Matches 22; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

Db 140 CTACATKGTGTTGGKMGATGATGATGAAGK 176
Cp 327 CTACCTCTGTTCTGTGAATCTTCTGAAGTAAAG 363

RESULT 8 C87905 337 bp mRNA EST 04-MAR-1998
LOCUS Mus musculus fertilized egg cDNA 3'-end sequence, clone J0253E04,
DEFINITION

ACCESSION mRNA sequence.
C87905
NID 92919862
KEYWORDS EST: EST(expressed sequence tag).
SOURCE Mus musculus (strain:C57BL/6J) fertilized one-cell-embryo cDNA to mRNA, clone_1lb:Mouse fertilized one-cell-embryo cDNA clone:J0253E04.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (sites)
AUTHORS Ko,M.S.H., Kitchen,J.R., Wang,X., Wang,X., Theat,T.A., Sun,T., and Depalma,G.E., Liang,Y., Kargul,G.J., Sharara,R., Paonessa,P.D. and Doi,H.
TITLE Systematic analyses of genes expressed in fertilized mouse eggs (The ERATO/Doi Project at Wayne State University)
JOURNAL Unpublished (1998)
REFERENCE 2 (bases 1 to 337)
AUTHORS Doi,H. and Ko,M.S.H.
TITLE Direct Submission
JOURNAL Submitted (21-JAN-1998) to the DDBJ/EMBL/GenBank databases. Hirofumi Doi, Doi Biosymetry Project, ERATO, Japan Science and Technology Corporation (JST); WBG Marine East 12F, 2-6 Nakase, Mihama-Ku, Chiba-shi, Chiba 261-7112, Japan (E-mail:hdoibioa.jst.go.jp, tel:81-43-299-1351, Fax:81-43-297-7530)
FEATURES
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/strain="C57BL/6J"
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/clone_1lb="Mouse fertilized one-cell-embryo cDNA"
/dev_stage="fertilized one-cell-embryo"

BASE COUNT 67 a 86 c 90 g 93 t 1 others
ORIGIN

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Best Local Similarity 77.1%; Pred. No. 1.05e-03;
Matches 27; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Cp 363 CCTTACTTCAGAGATTACAGAACAGAGGT 329

RESULT 9 A0134058 363 bp DNA GSS 22-SEP-1998
LOCUS HS-3056_A1_B09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3056 Col-17 Row-C, genomic survey sequence.
ACCESSION A0134058
NID 93525424
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homindaee; Homo.
REFERENCE 1 (bases 1 to 363)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Furlong,J., Shaker,R., Schmidt,S., Traicoff,R. and Hood,L.E.
TITLE Construction of a Characterized Clone Resource for Genomic Sequencing
JOURNAL Unpublished (1998)

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Sequence Tagged Connector
Plate: 3056 row: C column: 17

